

ID XX AAY28444 standard; protein; 1203 AA.
 AC XX AAY28444;
 DT 03-DEC-1999 (first entry)
 XX DE Human ptc-2 protein.
 XX KW Patched-2; ptc-2; human; hedgehog receptor; nontropic; neuroprotective;
 KW antiinflammatory; antiparkinsonian; cardiatic; antiarthritic; screening;
 KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
 KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
 KW graft; transplant; treatment; nervous system injury; chemical injury;
 KW vascular injury; infection; inflammatory; tumor-induced injury; ageing;
 KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
 KW Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis;
 KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
 KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
 KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
 KW lesion-induced death; neuron regeneration; damage repair; skeletal;
 KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
 KW prosthesis cartilage device; spermatogenesis; fertility enhancer.
 XX OS Homo sapiens.
 XX FN WO9929854-A1.
 XX PD 17-JUN-1999.
 XX PF 08-DEC-1998; 98WO-US026009.
 XX PR 08-DEC-1997; 97US-0067940P.
 XX PA (ONTO-) ONTOGENY INC.
 XX PI Bumcrot DA;
 XX DR WPI; 1999-561298/47..
 XX DR N-PSDB; AAX89478.
 XX PT New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
 PT prevention and/or reduction of the severity of neurological conditions.
 XX PS Claim 3; Page 73-77; 80pp; English.
 CC This invention describes a novel recombinantly produced human patched-2
 CC (ptc-2) polypeptide which has nontropic, neuroprotective, cardiac,
 CC antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
 CC protein is a hedgehog receptor and is therefore capable of modulating
 CC hedgehog signalling, and so affect a number of hedgehog-mediated
 CC biological activities. The human patched-2 (ptc-2) protein can be used to
 CC screen for modulators, antagonists and agonists, which are likely to play
 CC an important role in the modulation of cellular proliferation and
 CC maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
 CC tissues during disease states. Modulators of ptc-2 protein can be used
 CC for in vivo reformation of tissue; to improve grafting and morphology of
 CC transplanted tissue; for the treatment, prevention and/or reduction of
 CC the severity of neurological conditions deriving from: injury to the
 CC nervous system including traumatic injury, chemical injury, vascular injury
 CC and deficits (such as ischemia resulting from stroke), together with
 CC infectious/inflammatory and tumor-induced injury; ageing of the nervous
 CC system including Alzheimer's disease; chronic neurodegenerative diseases
 CC of the nervous system including Parkinson's disease, Huntington's chorea,
 CC amyotrophic lateral sclerosis, as well as spinocerebellar degenerations;
 CC and chronic immunological diseases of the nervous system including
 CC multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
 CC of autonomic disorders of the peripheral nervous system, including
 CC disorders affecting the innervation of smooth muscle and endocrine
 CC tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
 CC Antagonists of ptc-2 protein can be used to prevent differentiation of
 CC cells in culture, as well as for treatment of chronic pain syndromes.
 CC Agonists may be used to rescue neurons from lesion-induced death as well
 CC as neuron regeneration, in diseases such CNS trauma infarction, (viral)

CC infection, metabolic disease, nutritional deficiency, toxic agents, and
 CC so on. ptc-2 therapeutics may also be used for the repair of central and
 CC peripheral nerve damage, for repair and regeneration of non-neuronal
 CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
 CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
 CC for generation of prosthetic cartilage devices, and to induce
 CC spermatogenesis and as fertility enhancers. This sequence represents the
 CC human ptc-2 protein described in the invention
 XX SQ Sequence 1203 AA;

Query Match 99.8%; Score 6248; DB 2; Length 1203;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRSPRLRLPSYTPPARTAPQIILAGSKAPLMRAYFOGLLSLGGCIQRHCGKVLV 60
 DB 1 MTRSPRLRLPSYTPPARTAPQIILAGSKAPLMRAYFOGLLSLGGCIQRHCGKVLV 60
 QY 61 LGLLAFGALALGLRMAIETNLEQLWVEGVSQELHYTKELGEEAAYTSQMLIQTAR 120
 DB 61 LGLLAFGALALGLRMAIETNLEQLWVEGVSQELHYTKELGEEAAYTSQMLIQTAR 120
 QY 121 QEGENILTPBALGLHLQAALTASKVQVSLYKGSNDLNKI CYKSGVPLIENGMIENMKL 180
 DB 121 QEGENILTPBALGLHLQAALTASKVQVSLYKGSNDLNKI CYKSGVPLIENGMIENMKL 180
 QY 181 FPCVILTPDCFWGAKLQGGSAVLPGRPDITQWNLDPQLLELPGFASLEGGFRELDDK 240
 DB 181 FPCVILTPDCFWGAKLQGGSAVLPGRPDITQWNLDPQLLELPGFASLEGGFRELDDK 240
 QY 241 AQVGQAVYVGRPCLLHPDHLCPSPAPNHHSRQAPNVAHELSCGCHGFSGHKNHWEELLG 300
 DB 241 AQVGQAVYVGRPCLLHPDHLCPSPAPNHHSRQAPNVAHELSCGCHGFSGHKNHWEELLG 300
 QY 301 GMARDPOGELIRAEALOSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLAQWRFFV 360
 DB 301 GMARDPOGELIRAEALOSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLAQWRFFV 360
 QY 361 QLAQALPENASQOIHFASSTLDDILHAFSEVSAARVWGYLLMLAYACVTMLRWDCAQ 420
 DB 361 QLAQALPENASQOIHFASSTLDDILHAFSEVSAARVWGYLLMLAYACVTMLRWDCAQ 420
 QY 421 SQSGVGLAGVLLVALAVASGLICALLGITFNATTOVLPAFLAIGICVDVDFLLAHAFTE 480
 DB 421 SQSGVGLAGVLLVALAVASGLICALLGITFNATTOVLPAFLAIGICVDVDFLLAHAFTE 480
 QY 481 ALPGTPIQRMGECLORTGTSTVVLTSINNMAAFMAALVPIPALRAFSQAALVWGTFFV 540
 DB 481 ALPGTPIQRMGECLORTGTSTVVLTSINNMAAFMAALVPIPALRAFSQAALVWGTFFV 540
 QY 541 AVMLVFPAILSLDRLRRHQRDLVLCSSPSCSAQVITLPOBLGDTVPVGAHLTATV 600
 DB 541 AVMLVFPAILSLDRLRRHQRDLVLCSSPSCSAQVITLPOBLGDTVPVGAHLTATV 600
 QY 601 QAFTHCEASSQHVITLPPQALHVPDPSPGLSELPSPGSGSTEDLIGQBEETRQAACKS 660
 DB 601 QAFTHCEASSQHVITLPPQALHVPDPSPGLSELPSPGSGSTEDLIGQBEETRQAACKS 660
 QY 661 LPCARWLAHFARYQAPFLLQSHAKAIVLVFGALLGLSLYGATLVODGLALTVDVPRG 720
 DB 661 LPCARWLAHFARYQAPFLLQSHAKAIVLVFGALLGLSLYGATLVODGLALTVDVPRG 720
 QY 721 TKEAFLSAQLRYSLYSLYVALVTGGFDYAHQSQUALFDLHORFSSKAVLPPPTAQERT 780
 DB 721 TKEAFLSAQLRYSLYSLYVALVTGGFDYAHQSQUALFDLHORFSSKAVLPPPTAQERT 780
 QY 781 WLHYRNWLOGIAAFQDDWASGRITRHSYNGSGEDGALAYKLLIQTGDAQEPDFDSOLT 840
 DB 781 WLHYRNWLOGIAAFQDDWASGRITRHSYNGSGEDGALAYKLLIQTGDAQEPDFDSOLT 840
 QY 841 TRKLVDEGLIPPELFYWGTLVWVSSDFLGAASQANFYPPPEWLHKDYDTTCENLRIP 900

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Db 841 TRKLVREGILPPELFYMGILTVWSSDPLGLAASQANFYPPPEWLHDKYDTTCENLRIP 900
 QY 901 PAQPLEFAQPFLLRGLQKTDADFVEAIEGARAACAEAGQAGVHAYPGSGPFLFWEQVYGL 960
 Db 901 PAQPLEFAQPFLLRGLQKTDADFVEAIEGARAACAEAGQAGVHAYPGSGPFLFWEQVYGL 960
 QY 961 RRCFLAVCTLLVCTELVCAALLINPWTAGLIVLVLAMTVFELGIMGFLGKLSAIPVV 1020
 Db 961 RRCFLAVCTLLVCTELVCAALLINPWTAGLIVLVLAMTVFELGIMGFLGKLSAIPVV 1020
 QY 1021 ILVASGIGVEFVHVAGLITTOGSRNLRAAHLHTFAPVTDGALSTILGLMLAGSH 1080
 Db 1021 ILVASGIGVEFVHVAGLITTOGSRNLRAAHLHTFAPVTDGALSTILGLMLAGSH 1080
 QY 1081 FDFIVRYFFAALTVLLGLLHGLVLLPVLLSILGPPPEVIOMYKSPETILSPAPQGGG 1140
 Db 1081 FDFIVRYFFAALTVLLGLLHGLVLLPVLLSILGPPPEVIOMYKSPETILSPAPQGGG 1140
 QY 1141 LRWGASSLSQSPARVTTSTMTVAIHPPPLPGAVIHPADBPWPSPATSSGNLSRGPQP 1200
 Db 1141 LRWGASSLSQSPARVTTSTMTVAIHPPPLPGAVIHPADBPWPSPATSSGNLSRGPQP 1200
 QY 1201 ATG 1203
 Db 1201 ATG 1203

RESULT 5

ID AAY92703 standard; protein; 1203 AA.
 AC AAY92703;

DT 10-AUG-2000 (first entry)
 DE Human patched 2 (PTCH2) protein splice variant.
 KW Patched 2; PTCH2; 1p32-35; tumour suppressor; familial melanoma CMM1;
 KW familial adenomatous polyposis; hMcm1; Michelin Tire Baby Syndrome;
 KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
 KW basal cell carcinoma; gene therapy; chromosome 1p32-35; splice variant.
 OS Homo sapiens.

PN WO20020037-A1.
 XX 13-APR-2000.
 PF 06-OCT-1999; 99WO-SE001784.
 XX 06-OCT-1998; 98SE-00003393.
 PR (KARO-) KAROLINSKA INNOVATIONS AB.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PI Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
 XX Hollingsworth RE;
 DR NPI; 2000-303645/26.
 DR N-PSDB; AAA09084.

Isolated human protein capable of participating in human patched gene/Sonic hedgehog pathway during embryonic development is used in medicament for treatment of condition involving tumors such as basal cell carcinoma.

Disclosure; Page; 55pp; English.
 This protein is a splice variant encoded by the novel human patched 2 gene (PTCH2), which has been localized by radiation hybrid mapping to chromosome 1p32-35 with D1S211 and W11404 as closest flanking markers and with an estimated localisation 5.5 cR from D1S443. This region is often lost by LOH in various different tumour types, such as neuroblastoma,

CC melanoma and breast and colon cancer. PTCH2 is a candidate for a tumour suppressor gene in this region. It is also a candidate gene for involvement in familial melanoma CMM1, modifier locus for familial adenomatous polyposis hMcm1 and Michelin Tire Baby Syndrome. PTCH2 is capable of participating in the human patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic development and/or carcinogenesis. The isolated human protein is useful as a medicament for the treatment of a condition involving tumours such as BCC (basal cell carcinoma). The nucleic acid is useful in gene therapy, and for use as a probe, primer or a diagnostic agent. Note: This sequence was constructed using information from Figure 2B and the protein sequence given on pages 41-44 of the CC specification

XX Sequence 1203 AA;

Query Match 99.5%; Score 6238; DB 3; Length 1203;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1199; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRSPRLRLPSYTPPTAATAPOILAGSLKAPLMRAYFOGLLPSLGGCIQRHCGKVLF 60
 Db 1 MTRSPRLRLPSYTPPTAATAPOILAGSLKAPLMRAYFOGLLPSLGGCIQRHCGKVLF 60
 QY 61 LGLAFGALALCLRMALITETNLEQLWVEVGRSVSOELHYTKEKLEGEAAYSOMLIQTAR 120
 Db 61 LGLAFGALALCLRMALITETNLEQLWVEVGRSVSOELHYTKEKLEGEAAYSOMLIQTAR 120
 QY 121 QEGENILTPALGLHQAALTASKVQVSLYKSWDLNKICYKSGVPLTIENGMIEMIEKL 180
 Db 121 QEGENILTPALGLHQAALTASKVQVSLYKSWDLNKICYKSGVPLTIENGMIEMIEKL 180
 QY 181 PFCVILTDLDCFWEGAKLOGGSAYLPGRPDIQTNWLDPEOLLEELGPPFASLEGRELIDK 240
 Db 181 PFCVILTDLDCFWEGAKLOGGSAYLPGRPDIQTNWLDPEOLLEELGPPFASLEGRELIDK 240
 QY 241 AQVGQAVYGRPCLHPDDLHCPSPAPNHHSROAPNVAMHLSGGCHGFSKFMHWBEILLG 300
 Db 241 AQVGQAVYGRPCLHPDDLHCPSPAPNHHSROAPNVAMHLSGGCHGFSKFMHWBEILLG 300
 QY 301 GMARDPOGELLRAEALQSTFLMSPRQLYEHFRGDYQTHDIGNWSEBQASTVLQAWRRFV 360
 Db 301 GMARDPOGELLRAEALQSTFLMSPRQLYEHFRGDYQTHDIGNWSEBQASTVLQAWRRFV 360
 QY 361 QLAQEALPENASQOIHFASSTTLDILHAFSEVSAARVVGCGYLLMAYACVTLRWDCAQ 420
 Db 361 QLAQEALPENASQOIHFASSTTLDILHAFSEVSAARVVGCGYLLMAYACVTLRWDCAQ 420
 QY 421 SQGSVGLAGVLLVALAVASGLGALLGITFNAAITTOVLPFALGIGVDDVFLAHAFTE 480
 Db 421 SQGSVGLAGVLLVALAVASGLGALLGITFNAAITTOVLPFALGIGVDDVFLAHAFTE 480
 QY 481 ALPGTQERMGECLQRTGTSVVLTSSINNMAALVPIPALRAFSLQAAIVVGCTFV 540
 Db 481 ALPGTQERMGECLQRTGTSVVLTSSINNMAALVPIPALRAFSLQAAIVVGCTFV 540
 QY 541 AVMLVFPAILSLDLRRHRCORLVLCFSPSCSAQVIQILPQELGDTVPVGHATATV 600
 Db 541 AVMLVFPAILSLDLRRHRCORLVLCFSPSCSAQVIQILPQELGDTVPVGHATATV 600
 QY 601 QAETHCEASSQHVVTILPPOAHLVPPSPDPLSGSELPSPGSGTDLILCOBETQKAACKS 660
 Db 601 QAETHCEASSQHVVTILPPOAHLVPPSPDPLSGSELPSPGSGTDLILCOBETQKAACKS 660
 QY 661 LPCARNLHAHFARYQFAPLLQSHAKAIVLVLFGALLGLSLYCATLVQDGLATDVVRG 720
 Db 661 LPCARNLHAHFARYQFAPLLQSHAKAIVLVLFGALLGLSLYCATLVQDGLATDVVRG 720
 QY 721 TKEHAFSLQRLYFSLYEVALVTQGGFDYAHQSORALFDLHQRFSSLKAVLPPPTAPRT 780
 Db 721 TKEHAFSLQRLYFSLYEVALVTQGGFDYAHQSORALFDLHQRFSSLKAVLPPPTAPRT 780
 QY 781 WLHYENWLGQICAAFDQDQWASGRITRHSYRNGSEGALAYKLLIQTGAQBPPLFSQUT 840

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 08:02:01 ; Search time 5460 Seconds

(without alignments)

8028.754 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence:

1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US0990046/runat_21112004_130919_18544/app_query.fasta_1.1351
-DB=EST -QFMT=fastap -SUFFIX=rc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0990046_@CGN_1_1_3361_@runat_21112004_130919_18544 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2724	43.4	3868	9 AY415485	AY415485 Homo sapi
2	2708	43.2	3871	9 AY415487	AY415487 Mus muscu
3	2362	37.7	3950	9 AY415486	AY415486 Pan trogl
4	1097.5	17.5	711	7 CF733501	CF733501 UI-M-HB0
5	1071	17.1	708	7 CK830937	CK830937 4054508 B
6	1043	16.6	662	7 CF531700	CF531700 UI-M-FY0
7	1032	16.5	603	7 CN671167	CN671167 A0902E10-
8	1005	16.0	571	4 BM105989	BM105989 509593 MA
9	998	15.9	600	6 CA528868	CA528868 8091-13 M

10	988	15.8	625	7	CN676164	A0976A07-
11	970	15.5	911	5	BX844270	BX844270
12	959	15.3	974	5	BQ964086	AGENCOURT
13	905	14.4	639	2	BB612664	BB612664
14	891	14.2	573	2	B2334509	141639 MA
15	884	14.1	778	7	CK633185	CK633185
16	883	14.1	506	4	BG384338	303388 MA
17	881	14.0	796	7	CN537294	UI-M-HS0-
18	865	13.8	788	6	CB723145	UI-M-HS0-
19	863.5	13.6	832	7	CN536865	UI-M-HS0-
20	853.5	13.6	814	7	CN532855	UI-M-HS0-
21	844	13.5	633	4	BJ038661	BJ038661
22	839.5	13.4	590	7	CK388757	CK388757
23	837.5	13.4	746	7	CF741492	UI-M-HS0-
24	834.5	13.3	736	1	AUI25183	AUI25183
25	827	13.2	637	4	BJ029994	BJ029994
26	823	13.1	770	7	CK639136	UI-M-HS0-
27	818.5	13.1	761	7	CF744664	UI-M-HS0-
28	811.5	12.9	711	7	CN535086	UI-M-HS0-
29	811.5	12.9	789	6	CB723783	UI-M-HS0-
30	810.5	12.9	723	7	CK636036	UI-M-HS0-
31	805.5	12.8	812	7	CF745394	UI-M-HS0-
32	751.5	12.0	465	5	BQ557141	H4044C10-
33	749	11.9	702	7	CF735093	CF735093
34	734.5	11.7	637	6	BY727737	BY727737
35	732.5	11.7	731	7	CK781271	UI-M-HS0-
36	730.5	11.6	659	6	CB722633	UI-M-HS0-
37	726.5	11.6	736	7	CN536823	UI-M-HS0-
38	712	11.4	589	4	BJ067833	BJ067833
39	711	11.3	477	6	CA530713	C0301G07-
40	701.5	11.2	649	7	CN534794	UI-M-HS0-
41	701	11.2	751	7	CN535375	UI-M-HS0-
42	695	11.1	742	6	CB526181	UI-M-HS0-
43	691	11.0	626	7	CO432549	UI-M-HS0-
44	679.5	10.8	733	7	CR586364	CR586364
45	678	10.8	727	6	CA749673	UI-M-HS0-

ALIGNMENTS

LOCUS AY415485 3868 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens PTCH gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.

ACCESSION AY415485

VERSION AY415485.1 GI:39771444

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3868)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 3868)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

FEATURES Location/Qualifiers

source 1..3868

QY	706	LeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHisAla	725	Db	2991	GGCGCGTGTCCACTCTCTGTGGAGTGTGATGCTGGGGATCTGAGTTCGACTTCATT	3050
Db	1914	CGAGTCAGAGACGGCTTGACCTTACGGACATGTACCTCGGAACCCAGAAATATGAC	1973	QY	1085	Val-----	1085
QY	726	PheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGly	745	Db	3051	GTCAGNN	3110
Db	1974	TTTATTGTGCAATTCAAATACATTTCTTCTACAACTATATATAGTACCAGAA	2033	QY	1086	-----ArgTyrPhePheAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHis	1102
QY	746	GlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSerSer	765	Db	3111	NN	3170
Db	2034	GCA---GACTACCCGAATATCCAGCACTTACTTTTACGACCTACACAGGAGTTTTCAGTAAC	2090	QY	1103	GlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluValIleGln	1122
QY	766	LeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrioLeuHisTyrTyr	785	Db	3171	GGCTTGAACCGCTGCCACA-----CCCTCCCTGAGCCACCCCGAGCGTGGTCCGC	3224
Db	2091	GTGAAGTATGTCATGTTGGAAGAAACAAACAGCTTCCCAAAATGTGGCTGACACTTC	2150	QY	1123	MetTyr-----	1124
QY	786	ArgAsnTrpLeuGlnGlyIleGlnAlaPheAspGlnAspTyrAlaSerGlyArgIle	805	Db	3225	TTCGCCATGCCCGCGCCACACGACGACGAGGGTCTGATTCTCTCGACTCGGAGTATAGT	3284
Db	2151	AGAGACTGGCTTCAGGACTTCAGGATGCATTGACAGTACTGGGAAACCGGAAATC	2210	QY	1124	-----	1124
QY	806	ThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIle	825	Db	3285	TCCAGACACAGTGTCTAGGGCTCAGCGAGGAGCTTCGGCACTACGAGGCCCGCAGCGCC	3344
Db	2211	ATGCCAAACAATTACAAGATGGATCAGACGATGGCTTGGCTACAAATCTCCTGGTG	2270	QY	1124	-----	1124
QY	826	GlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuVal	845	Db	3345	CGGGAGGCCCTGCCCAACCAAGATGATCGTGAAGCCACAGAAACCCCGTCTTCCGCCAC	3404
Db	2271	CAAACCGCAGCGCGATAGCCCATCGACATCAGCCAGTTGACTTAACAGCGTCTGGTG	2330	QY	1125	-----LysGluSerPro	1128
QY	846	AspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSer	865	Db	3405	TCCACTGTGGTCCATCCCGAATCCAGGCATCACCCACCTCGAACCCGAGACGAGGCC	3464
Db	2331	GATCAGATGGCATCATTAATCCAGCGCTTCTACATCTACCTGACGGCTTGGGTGACG	2390	QY	1129	GluIleLeuSer-----ProProAlaProGlnGly-	1138
QY	866	SerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGluTrp	885	Db	3465	CACCTGGACTCAGGGTCCCTGCTCCCGAGCGGAAGCCAGACGCCCGCAGGAGCCCC	3524
Db	2391	AGACACCCCGTGTGTGCTGCCCTCCCGAGCCAAACATCCCGCCACACGACCAATGG	2450	QY	1139	-----GlyGlyLeu-	1141
QY	886	LeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnPro	904	Db	3525	CCGAGAGAGGCTTGTGGCCACCCCTTACAGCCGCGCAGAGAGCTTTTGAATTTCT	3584
Db	2451	GTCCACGACAAAGCGACTCATGCTGAAACAGGCTGAGAAATCCCGGACGAGGCC	2510	QY	1142	-----ArgTrpGly-	1144
QY	905	LeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheVal	924	Db	3585	ACTGAAGGGCATCTTGGGCCCTAGCAATAGGCGCCCTGGGGCCCTCGCGGGCCGTTCT	3644
Db	2511	ATCAGATATGCCAGTTCCTCTTACCTCAAGCGCTTGGCGGACACCTCAGACTTCTG	2570	QY	1145	-----AlaSerSerLeuProGlnSerPheAla	1154
QY	925	GluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAla	944	Db	3645	CACAACCTCGAACCACCGAGCGTCCACTGCGGCGAGCTCGTCCCGCGCTACTGCCAG	3704
Db	2571	GAGCAATGAAAAGTAAGACCATCTGCGACCACTATACGAGCTGGGGCTGTCCAGT	2630	QY	1155	ArgValThrThr-----SerMetThrValAlaIleHisProProProLeu	1169
QY	945	TyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPhe	964	Db	3705	CCCATCACCACCTGAGCGGCTTCTGCTCCGTGACTGTGCGCGTGCACCCCGCGCTGTC	3764
Db	2631	TACCCCAAGCGCTACCCCTCTCTCTTGGGAGCAGTACATCGGCCCTCCGCCACTGGCTG	2690	QY	1170	ProGlyAlaTyrIleHisPro	1176
QY	965	LeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu	984	Db	3765	CCTGGGCTGGCGGAACCCC	3785
Db	2691	CTGCTGTTCATCAGCGTGGTGTGGCTGCACATTCCTCGTGTGCGCTGTCTCTCTCTG	2750	RESULT 2			
QY	985	AsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPhe	1004	AY415487			
Db	2751	AACCCCTGGAGCGCGGATCATTTGTGATGTCTCTGGCGCTGATGACGCTGATGCTTC	2810	LOCUS			
QY	1005	GlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValIleLeuValAla	1024	DEFINITION	AY415487	3871 bp DNA linear GSS 17-DEC-2003	
Db	2811	GGCATGATGGGCTCATCGGAATCAAGCTCAGTCCGCGCTGGCGCTGCTATCTGATGCT	2870	Mus musculus PTCH gene, VIRTUAL TRANSCRIPT, partial sequence,			
QY	1025	SerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrGln	1044	genomic survey sequence.			
Db	2871	TCTGTGTGCAAGAGTGGAGTTCACCGTTCACGTTGCTTGGCTTTCGACGCCCATC	2930	ACCESSION	AY415487		
QY	1045	GlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAsp	1064	VERSION	AY415487.1	GI:39771446	
Db	2931	GGCGACAAGAACCCGAGCGCTGTGCTTGGCTGGAGCACATGTTTGCACCCGCTCTGAT	2990	KEYWORDS	GSS.		
QY	1065	GlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIle	1084	SOURCE	Mus musculus (house mouse)		
				ORGANISM	Mus musculus		
				REFERENCE	1 (bases 1 to 3871)		
				AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,		
					Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,		
					Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,		
					Adams, M.D. and Cargill, M.		
					Inferring nonneutral evolution from human-chimp mouse orthologous		


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Db      1680  GTACCCAG-GACAACTCAGCTGTCCAGAGCCGAGACACAGCTCTACAGGACCT 1738
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Db      1739  GCTCTCCCAAGTCTCAGACTCC-----AGCTCCCACTCTCGAGCCCTCGACCAA 1792
QY      665  gTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHisAl 685
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QY      685  alysalalleValLeuValPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaTh 705
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QY      705  rLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 725
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Db      2033  AGCA---GACTACCCGAATATCCAGCCTACTTTACGACCTTCATAAGAGTTTCAGCA 2089
QY      765  rLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTy 785
Db      2090  TGTGAAGTATGTATCTGTGGAGGAGAAACAAGCACTTCCCAAAATGTGGCTCACTT 2149
QY      785  rArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 805
Db      2150  TAGAGACTGGCTTCAGAGCTTCAGGACTTCAGGATTCATTTGACAGTGGGAAACTGG 2209
QY      805  eThrArgHisSerTyrArgAsnGlySerGlyAlaLeuAlaTyrLysLeuLeuI 825
Db      2210  CATGCCAAACAATTATAAAATGGATCAGTCAGGGGTCTCGCTTACAAACTCTCGT 2269
QY      825  eGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 845
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QY      845  lAspArgGluGlyLeuLeuProGluLeuPheTyrMetGlyLeuThrValTrpValSe 865
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QY      865  rSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGluTr 885
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QY      904  oLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 924
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QY      924  lGluAlalleGluClyAlaAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAl 944
Db      2570  GGAAGCCATAGAAAAAGTAGAGTCATCTGTAAACAATATACGAGCCTGGGACTGTCC 2629
QY      944  aTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 964
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QY      964  eLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLe 984
Db      2690  GCTGCTATCCATCAGCGTGGTGTGGCTGCGCTTCTAGTGTGGCAGCTCTCTCTCT 2749
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QY      1024  aSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrGl 1044
Db      2870  ATCTGTGGCATCGGAGTGGAGTTACCGCTCCACGTGGCTTTGGCCTTTCTGACAGCC 2929
QY      1044  nGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1064
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QY      1064  pGlyAlalleSerThrLeuLeuGlyLeuMetLeuAlaGlySerHisPheAspPheIl 1084
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QY      1121  ----- 1121
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QY      1121  ----- 1121
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QY      1122  -----GlnMetTyrLysGluSerProGlu-IleLeuSerProProA 1135
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QY      1135  laPro----- 1136
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QY      1159  -----SerMetThrValAlaIleHisProProProLeuProGly 1171
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RESULT 3

AY415486

LOCUS

DEFINITION

Pan troglodytes PTCH gene, VIRTUAL TRANSCRIPT, partial sequence,

Genomic survey sequence.

ACCESSION

AY415486

VERSION

AY415486.1

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 3950)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 3950)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1..3950
 /gene="PTCH"
 /locus_tag="HCM5573"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,44e-199 Length: 3950
 Score: 2362.00 Matches: 515
 Percent Similarity: 53.59% Conservative: 164
 Best Local Similarity: 40.65% Mismatches: 402
 Query Match: 37.66% Indels: 186
 DB: 9 Gaps: 17
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 DB 3 GGAGACAGTAAAGTCGTGAATTAATATATCTCCGACAGATGGAGAGGCTATG 62
 QY 110 TyrThrSerGlnMetLeuLeuGlnThrAlaArgGlnGluGlyGluAsnLeuThrPro 129
 DB 63 TTTAATCCTCAACTCATGATCAGACCCCTAAAGAAGAGGTCGTAATCTCCTGACCACA 122
 QY 130 GluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSerLeu 149
 DB 123 GAAGCGCTCCTCAACACCTGAGCTCGGCACCTCCAGCCGCGTGTCCACGTATACATG 182
 QY 150 TyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuLeuGlu 169
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 QY 170 AsnGlyMetIleGluTrpMetLeuGluLysLeuPheProCysValIleLeuThrProLeu 189
 DB 243 ACAGGTTTACATGATCAGATAAGAAATATCTTACCCCTGTGTGATTAATACACCTTGG 302
 QY 190 AspCysPheTrpGluGlyAlaLysLeuGlnGlyLysSerAlaTyrLeuProGlyArgPro 209
 DB 303 GACTGCTTCTGGGAAGGGCAAAATTAACAGTCTGGGACAGACATACCTCTNNNNNNNN 362
 QY 210 AspileGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluLeuGluGlyProPheAla 229
 DB 363 NNN 422
 QY 230 SerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGly 249
 DB 423 NNN 482
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Db 483 NNN 542
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 QY 408 TyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeu 427
 Db 960 NNN 1019
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 QY 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSer 609

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 Qy 610 SerGlnHisValValThrIleLeuProGlnAlaHisLeuValProProPro----- 627
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 Qy 628 -----SerAspProLeuGlySerGlnLeuPheSerProGlyGlySerThrArgAspLeu 645
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 Qy 726 PheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGly 745
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 Qy 1141 -----LeuArgTrpGly----- 1144
 Db 3585 NCTGAAGGGCATTTCTGGCCCTAGCAATAGGACCGCTGGGGCCCTCGGGGGCCGTTCT 3644
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 Db 3645 CACAACTCTGGAAACCCAGCGTCCACTGCCATGGGAGCTCCGTCGCGGCTACTGCCAG 3704
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DEFINITION  UI-M-HB0-ckb-n-01-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone
VERSION   CF733501
KEYWORDS  EST.
SOURCE    CF733501.1 GI:37629834
ORGANISM  Mus musculus (house mouse)

REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL   NIH-MSC http://mgc.nci.nih.gov/.
COMMENT   National Institutes of Health, Mammalian Gene Collection (MGC)
          Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: Dr. James Lin University of Iowa
          cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
          cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Distribution information can be found at
          http://genome.uiowa.edu/distribution/mouse1.html
          This clone was contributed by the Brain Molecular Anatomy Project
          (BMAP)

Seq primer: PYX-5.
FEATURES             Location/Qualifiers
     source           1..711
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57Bl/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30608088"
                     /tissue_type="whole eye"
                     /dev_stage="embryo 12.5,13.5,14.5 dpc"
                     /lab_host="DHI0B (T1 phage resistant)"
                     /clone_lib="NTH BMAP_HB0"
                     /note="Organ: Eye; Vector: PYX- Asc; Site 1: EcoR I;
                     Site 2: Not I; The library was constructed according
                     Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is TTAATGCAAGT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH)."

ORIGIN
Alignment Scores:
Pred. No.:      2,51e-87      Length:      711
Score:          1097.50      Matches:    214
Percent Similarity: 91.14%      Conservative: 2
Best local Similarity: 90.38%      Mismatches: 12
Query Match:    17.50%      Indels:    9
DB:             7           Gaps:      1

US-09-990-046-2 (1-1203) x CF733501 (1-711)

Qy      178 GluIysLeuPheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaIys 197
Db      3 GAGAAGCTTTCCCTGTGTGATCCACCCCGCTTGACTGCTCTGGGAGGAGCAAA 62
Qy      198 LeuGlnGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217

```

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Db      63 CTCACAGGGGCTCTGCTACTTGGCGGGCGCCCTGATATCCAGTGGACCAACCTGGAC 122
Qy      218 ProGluGlnLeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeu 237
Db      123 CCTCAGCAGTGTCTCGAGGAGCTGGGCCCTTTGCCCTCTCTGGAGGGCTTCGCGGAACGTG 182
Qy      238 LeuAspIysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAsp 257
Db      183 CTAGATAAGGCACAGGTGGGCGCAGCCTATGTGTGGGGGAGCCCTGTCTGGACCCCTGATGAC 242
Qy      258 LeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHis 277
Db      243 CCCCACTGTCCACCTAGTGTCTCCACCGGCACAGCAGGAGGCTCCCAATGTGGCTCAG 302
Qy      278 GluLeuSerGlyGlyCysHisGlyPheSerHisIlyPheMetHisTrpGlnGluGluLeu 297
Db      303 GAGCTGAGTGGGGGCTGCCATGGCTTCTCCACAAAGTTTCATGCATCGCAGGAGGAGCACTG 362
Qy      298 LeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArg----- 312
Db      363 CTACTAGGGGCAAGCAGCAGAGATCTCCAGGACAGCTGTGAGGTGGGCTCCCTGG 422
Qy      313 -----AlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrG1 330
Db      423 GACTTTGGGCAGAGCCCTTGCAGAGCACCTTCTCTCATGAGTCCCTGTCTGAGCTGTACGA 482
Qy      330 uHisPheArgGlyAspTyrGlnThrHisAspIleGlyTrpSerGluGlnAlaSerTh 350
Db      483 GCATTTCCGGGGCACTACCAACAGACATCATCGGCTGGAGGAGGAGGAGGAGGAGCAT 542
Qy      350 rValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAs 370
Db      543 GGTGCTGAGGCGCTGGGAGAGCGGCTTTGTGACAGTAGCCAGGAGGCTCTGCGGCGCAA 602
Qy      370 nAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeu-AspAspIleLeuHisAlaP 390
Db      603 CGGCTGCAGCAGATCCATGCTTCTCTCCACCAACCCCTGGATGACATCTCTGCGCGGT 662
Qy      390 heSerGluValSerAlaAlaArgValGlyGlyGlyTyrLeuLeuMet 405
Db      663 TCTCTGAAGTCAGCACCAACCCGCTGGGTANGAGGCTATCTGCTTATG 709

RESULT 5
CK830937 708 bp mRNA linear EST 04-MAR-2004
LOCUS 4054508 BARC 8BOV Bos taurus cDNA clone 8BOV_18P22 5', mRNA
DEFINITION sequence.
ACCESSION CK830937
VERSION CK830937.1 GI:45056596
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovinae; Bos.
REFERENCE 1 (bases 1 to 708)
          Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
          Matukumalli,L.K.
          Construction and Analysis of a cDNA Library Generated From
          Intestinal Muscle and Epithelial Tissues of Holstein Cattle
          Unpublished (2004)
          Contact: Richard G. Baumann
          Bovine Functional Genomics Lab
          ANRI
          BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
          Tel: 3015048604
          Fax: 3015048744
          Email: rbaumann@auri.barc.usda.gov
          Single pass sequencing. Bases called and trimmed with phred
          0.000925 using options -trim_alt '-trim fasta. Vector identified
          by cross_match using options -mismatch 12 -mismatch 12
          Plate: 18 row: P column: 22

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Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 708.

FEATURES

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organism="Bos taurus"  
ol_type="mRNA"  
train="Holstein"  
b_xref="taxon:9913"  
clone="890V_18P22"  
sex="Female"  
index_type="Epitheli  
ev_stage="Lactating,  
lab_host="DH10B TONa"  
clone_lib="BAC ARC"  

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```

//note=Organ: Intestine; Vector: pCMWSPORT6.1; Site_1:
//NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
//library in pCMWSPORT6.1, constructed from equimolar mRNA
//pools derived from 5 sources, 4 lactating intestinal, 1
//neonatal intestinal 4/5 Lactating, Proximal Duodenum,
//Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
//Duodenum, Jejunum, Distal Ileum.

```

ORIGIN

Alignment Scores:	5.83e-85	Length:	218
Pred. No.:	1071.00	Matches:	702
Score:	96.43%	Conservative:	4
Percent Similarity:	94.64%	Mismatches:	8
Best Local Similarity:	17.09%	Indels:	0
Query Match:	7	Gaps:	0
DB:			

US-09-990-046-2 (1-1203) x CK830937 (1-708)

QY	897	LeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGly	916
Db	12	CTTCGCATCCCGGGGGCCAGCCCTTGGAGTTGCCAGTTCCCTCTCCTCGCGCGC	71
QY	917	LeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGlu	936
Db	72	CTCCAGAGACTGCAGACTTCGTGGAGGCCATTGAGGGGGCCCGGGCAGCGTGTCTCG	131
QY	937	AlaGlyGlnAlaGlyValHisAlaIleProSerGlySerProPheLeuPheThrGluGln	956
Db	132	GCCAGCCAGCGCGGGTGCATGCTACCCAGCGGCTCCCCCTTCTCTTCGGAGGACG	191
QY	957	TyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPhe	976
Db	192	TACCTGGGCTCGCGCGCTGCTTCCTGCTGGCAGTCTGCATCTGCTGCTGTACTTTC	251
QY	977	LeuValCysAlaLeuLeuLeuLeuAsnProThrAlaGlyLeuIleValLeuValLeu	996
Db	252	CTGCTGTGCCCTGCTGCTGCTCAA CCCCTGGACGGCTGCGCTCATAGTACTGGTCTCG	311
QY	997	AlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAla	1016
Db	312	GCGATGATGACTGTGGAGCTCTTTGGCATCATGGGTTCTCTGGGCATCAACCTCAGTGCC	371
QY	1017	IleProValValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisVal	1036
Db	372	ATCCGGTGGTGATCTCTGTGGCCCTCATATGGCATCGGTGTCGAGTTTCACCGCTCAGGTG	431
QY	1037	AlaLeuGlyPheLeuThrThrGlnClySerArgAsnLeuArgAlaAlaHisAlaLeuGlu	1056
Db	432	GCTCTGGGCTTCCTGACCGCTCAGGTAGCCGAACTTCGGGGTGGCCGGGCCCTCGAG	491
QY	1057	HisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeu	1076
Db	492	CGACACATTTGCTCCAGTGACCGATGGGGCCATCTCCACGTTGTGTAGTCTGCTCATGCTT	551
QY	1077	AlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThr	1096
Db	552	GCTGGCTCCAAATTGACTTCACTCGTAAGGTACTCTTTGGTGGTGTGCAAACTACTTACA	611

Qy	1097	LeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyPro	1116
Db	612	CTCTGGGCTCTCCATGGGCTGTGCTGCTCGGTACTGTGTCCATCTGGGCCC	671
Qy	1117	ProProGluVal	1120
Db	672	CCACCAGAGGTG	683

RESULT 6

LOCUS	CF531700	662 bp	linear	EST 12-SEP-2003
DEFINITION	UI-M-FYO-csq-d-19-0-UI_r1 NTH BMAP_FYO Mus musculus cDNA clone IMAGE:30356154 5', mRNA sequence.			

ACCESSION CF531700
IMAGE:J0336134 3 , IIRKNA

VERSION	CF531700.1	GI:34583668
KEYWORDS	EST.	
SOURCE	Mus musculus	(house mouse)
ORGANISM	Mus musculus	

ORGANISM Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 662)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cqapbs-r@mail.nih.gov

Tissue procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project

Seq primer: pYX-5.

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FEATURES
source
Location/Qualifiers
1..862
    .organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="TMAGE:30356154"
    /tissue_type="whole brain"
    /dev_stage="embryo 13.5,"
    /lab_host="DH10B (r1 phage)"
    /clone_lib="NIH BMAP FYO"
    /note="Organ: Brain; Vector: pCMVcat"
    Site 2: Not I; The library was constructed from a total RNA from 12.5 day E14.5 embryos of B6D.F1/J mice.
    Bonaïdo, Lennon and Soares. 1996. Denatured RNA was fractionated on 1% agarose formaldehyde gels. First strand cDNA synthesis was performed using a primer containing a Not I site. The cDNA library size selected according to size exclusion chromatography with EcoR I adaptor, digested with EcoR I, and ligated directionally into pVX-Amp vector. The cDNA library sequence located between the EcoR I sites was sequenced using the primer 5'-GAGGAGGACAG-3'. This library was screened using a 1.2 kb cDNA probe from the Iowa Brain Anatomy Project.
    Developing Mouse Nervous System.
    Institute of Mental Health, University of Toronto.
    program coordinator "

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ORIGIN

Alignment Scores:		
Pred. No.:	1.67e-82	Length:
Score:	1043.00	Matches:
Percent Similarity:	94.03%	Conservative:
Best Local Similarity:	90.41%	Mismatches:
Query Match:	16.63%	Indels:
DB:	7	Gaps:
		662
		199
		8
		13
		0
		0
		0

US-09-990-046-2 (1-1203) x CF531700 (1-662)

Sun Nov 28 09:38:33 2004

Qy	593	IleAlaHisLeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSerSerGlnHis	612
Db	2	ATTGGCCACCTGACTGCCACCGTGCAAGCCTTACCCCACTGCGAAGCCAGCAGCAGCAT	61
Qy	613	ValValThrLeuLeuProGlnAlaHisLeuValProProSerAspProLeuGly	632
Db	62	GTAGTACCAATTTTGGCTCTCTCAAGCCACCTGCTGCTCCAGGTTCTGAGCCCACTGGGC	121
Qy	633	SerGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThr	652
Db	122	TCCGAATCTCTATAGCCTGGAGGTTCTACACGGACCTTCTCATCTCAGGAGAGGGGACA	181
Qy	653	ArgGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAla	672
Db	182	GGGCCACAGCGGGCCTGCAGGCCCTGCTGTCGCCACTGGCACTCTCGCCCAATTTTGCC	241
Qy	673	ArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeu	692
Db	242	CGCTATCAGTTTGACCTTTTACTGCTCCAGACACGAGCCAGGCCCTGGTGTGCTGTC	301
Qy	693	PheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAla	712
Db	302	TTTGGGGCTCTTTGGGCTCGAGCCTCTATGAGCCACCTTGGTACAAGATGGGCTGGCC	361
Qy	713	LeuThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArg	732
Db	362	CTGCAGATGTGTCCTTAGGGGCCACGAGGAACATGCTTCTCAGCGCCCACTCAGG	421
Qy	733	TyrPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSer	752
Db	422	TACTTCTCCCTGTACGAGGTGGCTCTAGTGACACAGGGTGGCTTTTGACTACGCCCACTCC	481
Qy	753	GlnArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProPro	772
Db	482	CAACCGCGCCCTCTTTGATCTGCACCAAGCGCTTCAGCTCCCTCAAGGCTGTGTCGCCCA	541
Qy	773	ProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIle	792
Db	542	CCTGCCACCCAGGCACCCCGACCTGGCTTCTACTACCGCAGCTGGCTACAGGGTATC	601
Qy	793	GlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsn	812
Db	602	CAGGCTGATTTTGAACAAGACTGGGTTCTGGCGCATCACTGCGCACTTACCGCAAC	661

RESULT 7	CN671167	603 bp	mRNA	linear	EST 17-MAY-2004
LOCUS	CN671167				
DEFINITION	A902E10-5 NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:A902E10 IMAGE:30767001 5', mRNA sequence.				

IMAG:507070015 ; mag:
ACCESSION CN671167
VERSION CN671167.1 GI:47437618

VERSION: CNO 7
KEYWORDS: FST

KEYWORDS	EST.	SOURCE
	<i>Mus musculus</i>	(house mouse)

SOURCE
ORGANISM

ORGANISMS

REFERENCE

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

•

FEATURES
SOURCE

```

Plate: A0902 row: E column: 10
Seq primer: M13 Reverse
High quality sequence stop: 603
POLYA=No.

Location/Qualifiers
1. 603
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129SV/EvTac"
/db_xref="niaEST:A0902E10-5"
/db_xref="taxon:10090"
/clone="NIA:A0902E10 IMAGE:30767001"
/sex="Male"
/tissue_type="Embryonic Stem Cell"
/cell_line="129.3 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome res. 11: 1553-1558 (2001). [PMID: 11541991]). ES cells were plated at density 3x10^4/cm2, on gelatin-coated plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 1000 U/ml Lif, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCATGCGAGCGCGCCGCTTTT-3'] from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.7 kb. The library was constructed by Yulan Piao."

```

ORIGIN

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

110 00 000 045-3 (1-1203) x CN671167 (1-603)

156	LeuAsnLysIleCysTyrLysSerGlyValProLeulleGluAsnGlyMetIleGluTrp	175
3	TTGAACAAGATCTGCTCAAAATCAGGGGTTCCCTTATTGAAAATGGGATGATCAGCGG	62
176	MetIleGluLysLeuPheProCysValIleLeuThrProLeuAspCysPheTrpGluGly	195
63	ATGATTGAGAAGCTGTTTCCCTGTGTGATCTCACCCCGCTTGACTGCTTCTGGGNAAGGA	122
196	AlaLysLeuGlnGlyGlySerAlaIatyrLeuProGlyArgProAspIleGlnTrpThrAsn	215
123	GCCAAATCCCAAGGGGGCTCTGCCTACTTTCGGCGCCGCCCTGTATATCCAGTGGACCAAC	182
216	LeuAspProGluGlnLeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheAsp	235
183	CTGAGACCTCAGCAGCTCTCGAGAGCTGGGCCCTTTGCCCTCTCTGAGGGGCTTCCGG	242

TITLE D-oxeripin, a novel inhibitor of histone deacetylase, induces transcriptional activation of mouse stem cells and early embryonic
JOURNAL Transcriptional analysis of mouse stem cells and early embryonic
COMMENT PLoS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@nslu.gsc.nia.nih.gov

```

QY 236 GluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisPro 255
Db 243 GAACCTGCTAGATAAGGACACAGGTGGGCCAGCCCTATGTGGGGGAGCCCTGTCTGGACCT 302
QY 256 AspAspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnVal 275
Db 303 GATGACCCCCACTGTCCACTAGTGTCTCCACCGGCACAGCAGGAGGAGGCTCCCAATGTG 362
QY 276 AlaHisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu 295
Db 363 GCTCAGGAGCTAGTGGGGCTGCCAATGGCTTCTCCCAAGTTCATGACATGGCAGGAG 422
QY 296 GluLeuLeuGlyGlyMetAlaArgAspProGlnGlyGlnLeuLeuArgAlaGluAla 315
Db 423 GAACCTGCTACTAGGGGGGCACAGCAGAGATCTCCAGGACAGCTGTGTAGGGCAGAGGCC 482
QY 316 LeuGlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAsp 335
Db 483 TTGCAGAGACCTTCTCTGCTCATGAGTCCCGCTCAGCTGTACGAGCAGCTTCCGGGGCGAG 542
QY 336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355
Db 543 TACCAGACATGATCGCTGGAGCGGAGGAGGAGCCAGCATGTGTGCTGAGGCGCTGG 602

RESULT 8
BM105989
LOCUS 571 bp mRNA linear EST 21-NOV-2001
DEFINITION 509593 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM105989
VERSION BM105989.1 GI:17037059
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 571)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrnenkug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perteira,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keefe,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGG
Plate: 102 row: B column: 18
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1 . 571
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/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="vector: pcMV SPOR6; Site:1: NotI; Site:2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

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ORIGIN

Alignment Scores:

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Pred. No.: 3,29e-79 Length: 571
Score: 1005.00 Matches: 184
Percent Similarity: 98.95% Conservatives: 4
Best Local Similarity: 96.84% Mismatches: 2
Query Match: 16.02% Indels: 0
DB: 4 Gaps: 0

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US-09-990-046-2 (1-1203) x BM105989 (1-571)

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QY 770 LeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeu 789
Db 1 CTGCCCCCAACCCGGCCACCCAGGACCCCGACCTGGCTGCTACTTACCGCAGCTGGCTA 60
QY 790 GlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSer 809
Db 61 CAGGGAATCCAGCTGCAATTGACAGGACTGGGCTTCTGGGGCGCATACCCGCCACTCA 120
QY 810 TyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAsp 829
Db 121 TACCGCAATGGCTCTGAGGATGGGCCCTGGCATACAGCTGCTCGTCCAGACCCGGGAT 180
QY 830 AlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGly 849
Db 181 GCGCCAGGAGCCCTCTAGATTTTCAGCCAGCTGACCAAGAGCTGGTGACAAAGAGGG 240
QY 850 LeuIleProGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeu 869
Db 241 CTGATCCCAACCCGAGCTCTTTACATGGGGCTGACCGGTGGGTGAGCAGTACCCCTG 300
QY 870 GlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGluTrpLeuHisAspLys 889
Db 301 GGTCTGGCAGCTCACAGGCCAACTTCTATCCCCACCTCTGAGTGGCTGCATGACCAAG 360
QY 890 TyrAspThrThrGlyGluAsnLeuArgIleProProAlaGlnProLeuGluPheAlaGln 909
Db 361 TATGACACCAACCCGGGAGAACTTTCGATCCCGCGCGCCAGCCCTTGGAGTTTGCCAG 420
QY 910 PheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGly 929
Db 421 TTCCTTCTCCTCGCGCGGCTCCAGAAAGACTCCAGACTTTCGTGGAGGCCATTGAGGG 480
QY 930 AlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySer 949
Db 481 GCGCGGCGAGCGTGTGCTGAGCCAGCCAGCGGGGTGCATGCTACCCCGCGGCTCC 540
QY 950 ProPheLeuPheTrpGluGlnTyrLeuGly 959
Db 541 CCCTTCTCTTCTGGGAGCAGTACCTGGGC 570

RESULT 9
CA528868
CA528868
LOCUS 8091-13 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION CA528868
VERSION CA528868.1 GI:25042932
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 600)
AUTHORS Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
TITLE Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)
MEDLINE 21671825
PUBMED 11812828
COMMENT Contact: Klein WH

```

Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES

source
Location/Qualifiers
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue type="neural retina"
/dev stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

Alignment Scores:
Pred. No.: 1,5e-78 Length: 600
Score: 998.00 Matches: 190
Percent Similarity: 97.49% Conservativeness: 4
Best Local Similarity: 95.48% Mismatches: 5
Query Match: 15.91% Indels: 0
DB: 6 Gaps: 0

US-09-990-046-2 (1-1203) x CA528868 (1-600)

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QY 829 AspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLyLeuValAspArgGlu 848
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Db 3 AATGCCAGGAGCCTCTGATTTACGCCAGCTGACCAAGAAATCTGTGGACAAAGGAG 62

QY 849 GlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTyrValSerSerAspPro 868
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Db 63 GGACTCAATCCCCAGAGCTCTTACATGGGGCTTAACCGTGTGGTGAGCAGCAGCCCC 122

QY 869 LeuGlyLeuAlaAspSerGlnAlaAsnPhetYrProProProGluTyrTrpLeuHisAsp 888
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Db 123 CTGGCCCTCGCAGCTCTCAGGCCAACTTCTACCCCCCACTCCAGAGTGGCTTCAAGAC 182

QY 889 LysTyrAspThrThrGlyGluAsnLeuArgIleProProAlaGlnProLeuGluPheAla 908
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 183 AAATATGATACCACCGGGGAGAACCTTGCATCCCGCAGCCCTGTGAGTTGGC 242

QY 909 GlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGlu 928
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Db 243 CAGTTCCCTTCTCTGTCATGAGTCTCAGAGACTGCGAGACTTGTAGAGCCATCGAA 302

QY 929 GlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGly 948
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Db 303 GGGGCCAGGGCGCATGCACAGAGGAGGCGAGGCGGCTGCATGCTACCCCAAGTGGC 362

QY 949 SerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaVal 968
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Db 363 TCCCTCTCTCTCTCTGGGAGCAGTATCTGGGCTTTCGGCGCTCTCTCTCTCTGGCAGTC 422

QY 969 CysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTyrThr 988
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 423 TGCATCTTCTGTGTGTGTCACCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482

QY 989 AlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGly 1008
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Db 483 GCTGGCCTCATAGTCTGGTCTGGCAATGATGACTGTGGAGCTCTTGTGTATATGGA 542

QY 1009 PheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSerValGly 1027
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Db 543 TTCTGGGCATCAAACTAGTGTGCATCCCGTGGNAATCTCGNGCCCTCTATAGGC 599

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RESULT 10

LOCUS CN676164 625 bp mRNA linear EST 17-MAY-2004
DEFINITION A0976A07-5 NIA Mouse Embryonic Stem (ES) cell (Lif+), 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:A0976A07
IMAGE:30774054 5', mRNA sequence.
ACCESSION CN676164
VERSION CN676164.1 GI:47442615

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 625)

REFERENCE

AUTHORS
Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,
VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Basse, U.C.,
Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L.,
Tanaka, I.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,
Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,
Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A.,
Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,
D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

TITLE

Transcriptome analysis of mouse stem cells and early embryos

JOURNAL

PLoS Biol. 1 (3), 410-419 (2003)

COMMENT

Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: A0976 row: A column: 07
Seq primer: M13 Reverse
High quality sequence stop: 625
POLYA-No.

FEATURES

source

Location/Qualifiers

1..625
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/EvTac"
/db_xref="niaEST:A0976A07-5"
/db_xref="taxon:10090"
/clone="NIA:A0976A07 IMAGE:30774054"
/sex="Male"
/tissue type="Embryonic Stem Cell"
/cell_line="129.3 ES cells"
/lab host="DH10B"
/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [pMID: 11544199]). ES
cells were plated at density 3x10⁴/cm² on gelatin-coated
plates and cultured for 48 hrs at 37 °C, 5% CO₂. Culture
medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,
0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
beta-mercaptoethanol, 1000 U/ml LIF, 100 U/ml penicillin,
and 100 ug/ml streptomycin. Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3'] from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to ligo-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.7 kb. The library was
constructed by Yulan Piao."

ORIGIN

Alignment Scores:
Pred. No.: 1,26e-77 Length: 625
Score: 998.00 Matches: 194
Percent Similarity: 96.63% Conservativeness: 7
Best Local Similarity: 93.27% Mismatches: 7


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Db      568 CAAGTGTATGATGAAATCTTGGACCTGAATCAAAATCTCTTAATAATCTGGAGTT 627
Qy      166 ProLeuLeuGluAsnGlyMetIleGluTrpMetIleGluLysLeuPheProCysValile 185
Db      628 CCAATTATGAAATGGCAATGATGAGAGGATGATTGAGAACTTTTCCCTTGTGTAATA 687
Qy      186 LeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlySerAlaTyrIleu 205
Db      688 ATTACACCTCTGGACTGTTTTTGGGAAGATCCCAAGCTTCAAGGTGGCTCTGSCATATCTA 747
Qy      206 ProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluLeu 225
Db      748 CCAGGAAGAGCTGACATTCATGAGCAACCTAGATCCCATCAAGTTCATGGAAGAGCTT 807
Qy      226 GlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGln 245
Db      808 GGTCACTTCCAGCTCTTGATGGCTTCAAGGAATGCTGGACAAGGCTGAAGTAGGACAG 867
Qy      246 AlaTyrValGlyArgProCysLeuHisProAspAsp 257
Db      868 GGATATATGGAACGACCTTGTCTGGACCTACAGAC 903

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RESULT 12
BQ964086
LOCUS   BQ964086
DEFINITION AGENCOURT 10054944 NIH_MGC_134 Mus musculus cDNA clone
IMAGE: 6509228 5', mRNA sequence.
ACCESSION BQ964086
VERSION   BQ964086.1 GI:22379564
KEYWORDS EST.
SOURCE    Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 974)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM14076 row: C column: 21
High quality sequence stop: 689.

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FEATURES

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Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6509228"
/tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_134"
/notes="Vector: pCMV-Sport6.1; Site 1: EcoRV; Site 2: NotI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC library."

```

ORIGIN

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Alignment Scores:
Pred. No.: 1,01e-74 Length: 974
Score: 959.00 Matches: 199
Percent Similarity: 67.05% Conservative: 35
Best Local Similarity: 57.02% Mismatches: 76
Query Match: 15.29% Indels: 39
DB: 5 Gaps: 4

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US-09-990-046-2 (1-1203) x BQ964086 (1-974)
Qy      848 GluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTprValSerSerAsp 867
Db      28 GATGGCATCATTAATCCGAGCGCTTCTATCATCTACTGACCGCTGGGTGGTCAACAGAC 87
Qy      868 ProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrpIleuHis 887
Db      88 CTTGTAGCTTACGCTGCTCCAGGCCAACATCCGGCTCACCAGCGCGGAGTGGTCCAT 147
Qy      888 AspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGlu 906
Db      148 GACAAAGCCGACTACATGCTCCAGAGACCCAGGCTGAGAATCCAGAGCAGAGCCATCCAG 207
Qy      907 PheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAla 926
Db      208 TACGCTCAGTTCCCTTCTTACCTCAAGGCCCTACAGACACCTCAGACTTTTGTGAAGCC 267
Qy      927 IleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrPro 946
Db      268 ATAGAAAAGTGAGAGTCACTCTGAACAACTATACAGCCTGGGACTGTCCAGCTTACCCT 327
Qy      947 SerGlySerProPheLeuPheTrpGluGlnTrpLeuGlyLeuArgArgCysPheLeuLeu 966
Db      328 AATGCTACCTCTTCTCTTCTGGAGCAGTACATCAGCCTGGCCACTGCTGCTGTGCTA 387
Qy      967 AlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnPro 986
Db      388 TCCATCAGCGTGGTCTGGCTGCACGTTCTAGTGTGGCAGTCTTCTCTCTGAACCCC 447
Qy      987 TrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGlyIle 1006
Db      448 TGGAGCGCGGGATCATTTGTCATGCTGCTGCTGTGATGACCGTTGAGCTCTTTGGCATG 507
Qy      1007 MetGlyPheLeuGlyIleLysLeuSerAlaIleProValIleValIleValAlaSerVal 1026
Db      508 ATGGCCCTCATCGGGATCAAGCTGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 567
Qy      1027 GlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySer 1046
Db      568 GGCATCGGAGTGGAGTTACCGCTCCAGCTGGCTTTGGCCCTTCTGACAGCCATTTGGGAC 627
Qy      1047 ArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGlyAla 1066
Db      628 AAGAACCACAGGGCTATGCTGCTCTGGAGCACATGTTTGTCTCCCGCTTCTGGACGGTGT 687
Qy      1067 IleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArg 1086
Db      688 GTGTCCACTCTCTGCTGGGTACTGATGCTTGGAGGCTCCGAAATTGATTTTCATGTCAGA 747
Qy      1087 TyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeu 1106
Db      748 TACTCTTTTGGCGTCTCTGGCCATTCTCAGCGTCTTGGGGGTCTCAATGAGCTGTCTTG 807
Qy      1107 LeuProValLeuLeuSerIleLeuGlyProProProGluValIleGlnMetTyrLysGlu 1126
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Qy      1127 SerProGluIleLeuSerProProAlaProGlnGlyGlyLeuArgTrpGlyAlaSer 1146
Db      844 -----TGAGGGGTCTCC 855
Qy      1147 SerSerLeuProGlnSerPheAlaArgValThrSerMetThrValAlaIleHis-Pr 1166
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Qy      1166 oProProLeuProGlyAlaTyrIleHisProAlaProAspGluProProTrpSerPro--- 1185
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/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in

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ACCESSION BE234509
VERSION BE234509.1 GI:9019227
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE 1 (bases 1 to 573)
AUTHORS Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J., and Keefe, J.W.
TITLE Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
JOURNAL Mamm. Genome 13 (8), 475-478 (2002)
MEDLINE 22213789
PUBMED 12226715
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 79 row: 0 column: 17
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
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/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
ORIGIN
Alignment Scores: 5.15e-69 Length: 573
Pred. No.: 891.00 Matches: 173
Score: 92.67% Conservative: 4
Percent Similarity: 90.58% Mismatches: 14
Best Local Similarity: 14.21% Indels: 0
Query Match: 2 Gaps: 0
DB: 2
US-09-990-046-2 (1-1203) x BE234509 (1-573)
QY 502 ValValLeuThrSerLeuAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIle 521
Db 1 GTCCGCTCAGTCCATCAACATGTTGGCTTTCTATGCGCGCTCGTGGCCATC 60
QY 522 ProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAla 541
Db 61 CCTGCCCTGGCGCTTCTCTTGCAGCGCGCATAGTGTGCTGCACTTTCGAGCC 120
QY 542 ValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArg 561
Db 121 GTGATGTTGTCTTCGCGCGCTCTCAGCTGGACCTGCACCGCGCCACTGCCAGCGC 180
QY 562 LeuAspValLeuCysCysPheSerProCysSerAlaGlnValIleGlnIleLeuPro 581
Db 181 CTTGATGTCTCTGCTCTTGCAGCGCTGCTCTGCTGGGTGATTCAGATTCGCC 240
QY 582 GlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGln 601
Db 241 CAGGAGCTGGGGATGGAGACAGTACCCGCTGGGCATTGCCCGCTTGAAGCCAGCTTCAA 300

QY 602 AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAla 621
Db 301 GCCTTGTCCCTGTGAAGCCAGCAGCAGCATGTGCTCACCATCTTCCTCCCAACC 360
QY 622 HisLeuValProProProSerAppProLeuGlySerGluLeuPheSerProGlyGlySer 641
Db 361 CACCTGTGCCCCCACCCTTCTGACCTCTGCGCTCTGAGCTCTTCAGCCCCGGAGGTCC 420
QY 642 ThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeu 661
Db 421 ACAGGGACCTTCTAGGCCAGAGAGGGACACGGCAGGAGCGCTGCAAGTCCCTG 480
QY 662 ProCysAlaAlaArgTyrAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeu 681
Db 481 TCCTGTGCCCACTGGAATCTTGCCCAATTCGCCGCTCTCAGTTTGCACCTTGTGCTC 540
QY 682 GlnSerHisAlaLysAlaIleValLeuValLeu 692
Db 541 CAACCCATGCCAAGGCCATGCTGTGTAATT 573
RESULT 15
CK639185 778 bp mRNA linear EST 28-JAN-2004
LOCUS UI-M-H00-cnx-o-06-0-UI.r1 NIH_BMAP_H00 Mus musculus cDNA clone
DEFINITION IMAGE:30638069 5', mRNA sequence.
ACCESSION CK639185
VERSION CK639185.1 GI:41365051
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 778)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1..778
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30638069"
/tissue_type="Upper Head"
/dev_stage="9.5-10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_H00"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
ORIGIN

Alignment Scores:

Pred. No.:	3.56e-68	Length:	778
Score:	884.00	Matches:	165
Percent Similarity:	83.72%	Conservative:	51
Best Local Similarity:	63.95%	Mismatches:	38
Query Match:	14.09%	Indels:	4
DB:	7	Gaps:	3

US-09-990-046-2 (1-1203) x CK639185 (1-778)

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QY 279 LeuSerGlyGlyCysHisGlyPheSerHisPheMetHisTrpGlnGluLeuLeu 298
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Db 7 TTGAATGGTGGATGTCAGGTTTATCCAGGAAGTATATGTCATTCGCGAGGAGTTCATT 66

QY 299 LeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSer 318
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Db 67 GTGGTGGTACCGTCAAGAAATGCCACTGGAAATCTTGTCAGCGCTCACGCCCTGCAAAAC 126

QY 319 ThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---AspTyrGln 337
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Db 127 ATGTTCCAGTTAATGACTCCCAAGCAATGTATGAACACTTCAGGGCTACGACTATGTC 186

QY 338 ThrHisAspIleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArg 357
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 TCTCAC---ATCAACTGGAATGAAGACAGGCAGCCCATCTCGGAGGCTCGCAGAGG 243

QY 358 ArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAla 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 ACTTAGCTGGAGGTGTTTCATCAAGTGTGCGCCCAAACTCCACTCAAAAGGTTCTTCCC 303

QY 378 PheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArg 397
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 304 TTCACAACACGACCCCTGGACGACATCCTAAATCCTTCTTGATGTCTAGTGTATCCGA 363

QY 398 ValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAsp 417
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 364 GTGGCCAGCGGTACCTACTGATGCTTGCTATGCTGTTTAAACCATGCTGGCTGGGAC 423

QY 418 CysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaVal 437
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 424 TGCTCCAGTCCAGGTCGCGGGGCTGGCTGGCTGCTGTTGGTTCGCTGTCTCAGTG 483

QY 438 AlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGln 457
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 GCTGAGGATTCGGCTCTGCTCTTGTATGGCATTTCTTTAATGCTGCGCAACTCAG 543

QY 458 ValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAla 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 544 GTTTTGGCGTTTCTTGCTCTTGCTGTTGGTGGATGATGTTCTCTCTGGCCCATGCA 503

QY 478 PheThrGluAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGluCysLeu 495
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 604 TTCAGTGAACAGACAGACAGAAATAAGAGGATTCATTGAGGACAGGACTGGGAGTGCCTC 663

QY 496 GlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMet 515
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 664 AAGCGACCGGAGCGAGCGTGGCCCTCACCCTCCATCAGCAATGTCACCGCCTTCTTCATG 723

QY 516 AlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle 533
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 724 GNCGATTGATCCCTATCCCTGCGCTGCGAGGTTCTCCCTCCAGGCTGCTGTG 777
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Search completed: November 22, 2004, 12:06:09
Job time : 5506 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 07:43:25 ; Search time 25 Seconds
(without alignments)
4629.951 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPPLRLPPSYTPPART.....SPAATSSGNLSRGPATG 1203
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5599	89.3	1182	2 T13952	membrane protein p
2	4042.5	64.5	1220	2 T18291	patched protein -
3	3340	53.3	1442	2 T18538	transmembrane prot
4	3337	53.2	1434	2 T30172	membrane protein p
5	1961.5	31.3	1299	1 S06119	hypothetical prote
6	1708.5	27.2	1405	2 T27969	hypothetical prote
7	992	15.8	714	2 T16126	hypothetical prote
8	603.5	9.6	1278	2 T30188	Niemann-Pick C dis
9	514	8.2	1055	2 T05663	hypothetical prote
10	465.5	7.4	955	2 T21612	hypothetical prote
11	444	7.1	933	2 T25600	hypothetical prote
12	444	7.1	1003	2 T26746	hypothetical prote
13	430.5	6.9	1015	2 T15830	hypothetical prote
14	416.5	6.6	889	2 T29590	hypothetical prote
15	389.5	6.2	936	2 T26521	hypothetical prote
16	386.5	6.2	956	2 A89153	hypothetical prote
17	380.5	6.1	1170	2 S92525	protein C24B5.3 [i
18	343.5	5.5	845	2 T25657	probable membrane
19	340	5.4	881	2 T31739	hypothetical prote
20	317.5	5.1	800	2 T26683	hypothetical prote
21	314	5.0	877	2 T24097	hypothetical prote
22	309	4.9	820	2 T32908	hypothetical prote
23	300	4.8	983	2 T21213	hypothetical prote
24	293.5	4.7	1456	2 T15961	hypothetical prote
25	291	4.6	840	2 T33217	hypothetical prote
26	275.5	4.4	871	2 T28706	hypothetical prote
27	261.5	4.2	890	2 T22186	hypothetical prote
28	258.5	4.1	690	2 T23359	hypothetical prote
29	188	3.0	1276	2 T18526	SREBP cleavage act

ALIGNMENTS

RESULT 1

T13952
membrane protein ptch2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13952
R:Motoyama, J.; Takabatake, T.; Takeshima, K.; Hui, C.
A:Title: Ptch2, a second mouse. Patched gene is co-expressed with Sonic hedgehog.
A:Reference number: Z17830; MUID:98122566; PMID:9462734
A:Accession: T13952
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1182 <MOT>
A:Cross-references: UNIPROT:O35595; EMBL:AB010833; PIDN:BAA24691.1
A:Experimental source: strain BALB/cCrSlc
C:Genetics:
A:Gene: ptch2
C:Superfamily: Drosophila membrane protein patched
C:Keywords: transmembrane protein

Query Match	89.3%	Score	5599;	DB	2;	Length	1182;
Best Local Similarity	90.9%	Pred. No.	0;				
Matches	1074;	Conservative	43;	Mismatches	64;	Indels	0;
Gaps	0;						
Qy	1	MTRSPPLRLPPSYTPPARTAAPQILAGSLKAPLWLRAYFOGLAFSLGCGIQRHCGKVLIF	60				
Db	1	MVRPLSLGELPPSYTPPARSAPHILAGSLQAPLWLRAYFOGLAFSLGCGIQRHCGKVLIF	60				
Qy	61	LGLAFGALALGLRMAIETNLEQLWVEGSRVSOELHYTKEKLGEAAAYTSQMLIQTAH	120				
Db	61	LGLVAFGALALGLRVAVIETDLEQLWVEGSRVSOELHYTKEKLGEAAAYTSQMLIQTAH	120				
Qy	121	QEGENILTPALGLHQAALTASKVQVSLYCKSWDLNKKIYKSGVPLIENGMIEMIEKL	180				
Db	121	QEGGNVLTPEALDLHLQAALTASKVQVSLYCKSWDLNKKIYKSGVPLIENGMIEMIEKL	180				
Qy	181	FPVILTPDLDFWEGAKLQGSAYLPGRPDIQTNLDPQLLELGFASLEGRELLDK	240				
Db	181	FPVILTPDLDFWEGAKLQGSAYLPGRPDIQTNLDPQLLELGFASLEGRELLDK	240				
Qy	241	AQVQAYVGRPCILHCPDPPSAPNHHRSQAPNVAHELSCGGCHGFHKFMHWQEEILLG	300				
Db	241	AQVQAYVGRPCILHCPDPPSAPNHHRSQAPNVAHELSCGGCHGFHKFMHWQEEILLG	300				
Qy	301	GMARDPQGLLRABALQSTFLLMSPOLYEHFRGDYQTHDIGWSEBOASTVLQAWQRRFV	360				
Db	301	GTARDLQGLLRABALQSTFLLMSPOLYEHFRGDYQTHDIGWSEBOASTVLQAWQRRFV	360				
Qy	361	QLAQEALPENASQOIHAFFSSTLLDDILLHAFSEVSAARVVGILLMLAYACVTMLRWDCAQ	420				
Db	361	QLAQEALPENASQOIHAFFSSTLLDDILLHAFSEVSTTRVVGILLMLAYACVTMLRWDCAQ	420				

probable efflux tr
transport protein
acriflavine resist
F09G8.3 protein -
hypothetical prote
probable antibioti
hypothetical prote
related to SREBP c
probable multi-dru
acriflavin resista
probable RND efflu
probable export pr
conserved hypothet
hypothetical membr
hypothetical prote

421 SQSGVLGAVLLVALAVASGLGICALLGITNAATQVLPALAGIGVDDVFLAHAPTE 480
421 SQGAVGLGAVLLVALAVASGLGICALLGITNAATQVLPALAGIGVDDVFLAHAPTE 480
481 ALPGTFLQRMGECLORTGTSVLTSTINMAAFMAALVPIPALRAFSLQAAIVVGCFTV 540
481 APPDTPLPERMGECURSTGTSVLTSTINMAAFMAALVPIPALRAFSLQAAIVVGCNFA 540
541 AVMLVFPAILSLDLRRRCORLDVLCFSPSCSAQVQIQLPQELGDTVPVGVIAHLTATV 600
541 AVMLVFPAILSLDLRRRRQRDLVLCFSPSCSAQVQIQLPQELGDRVPPVGVIAHLTATV 600
601 QAFTHCEASSQHVVTILPQAHLLVPPSPDPLGSELFPSPGGSTRDLGQEBETROKAACKS 660
601 QAFTHCEASSQHVVTILPQAHLLVPPSPDPLGSELFPSPGGSTRDLGQEBETROKAACKP 660
661 LPCARWNLAHAFARYQAFAPLLQSHAKATVVLVFGALLGLSLYGATLVODGALTDVVRPG 720
661 LCAHWTUAFARYQAFAPLLQTRAKALVLLVFFGALLGLSLYGATLVODGALTDVVRPG 720
721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPTAQAPT 780
721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPTAQAPT 780
781 WLHYRNWLOGIOAFDQDQWASGRITRHSYRNGSEGDALAYKLLIOTGDAQEPLDFSQIT 840
781 WLHYRNWLOGIOAFDQDQWASGRITRHSYRNGSEGDALAYKLLIOTGDAQEPLDFSQIT 840
841 TRKLVDRGLLPELFPYMGTLVWSSDPLGLAASQANFVPPPEWLHDKYDTTGNLRIP 900
841 TRKLVDRGLLPELFPYMGTLVWSSDPLGLAASQANFVPPPEWLHDKYDTTGNLRIP 900
901 PAQPLEFAQFPFLGLGLOKTDVFAIEGARAACAGVAVHVPSPGPFLEWQYGLG 960
901 AAQPLEFAQFPFLGLGLOKTDVFAIEGARAACAGVAVHVPSPGPFLEWQYGLG 960
961 RRCFLLAVCILLVCTFLVCAILLNPNWAGLIVLVAMTWELFGIMGLGKLSAIPV 1020
961 RRCFLLAVCILLVCTFLVCAILLNPNWAGLIVLVAMTWELFGIMGLGKLSAIPV 1020
1021 ILVASVGIGVEFTVHVALGFTTQGSRLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
1021 ILVASIGIGVEFTVHVALGFTSHGSRNLRAASLEQIFAPVTDGAVSTLLGLMLAGSN 1080
1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOYKESPEILSPAPQGG 1140
1081 FDFIVRYFFVLTVLTLGLLHGLLPLVLLSILGPPPVQVQYKESPTLNSAAPQGG 1140
1141 LRWGASSLPQSFAFVTTSMVAIHPPPLPGAYIHPADPEP 1181
1141 LRWDRPPTLQSFARVTTSMVALHPPPLPGAYVHPASEP 1181

RESULT 2
T18291
patched protein - zebra fish
C:Species: brachydanio rerio (zebra fish)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18291
R:Concordet, J.P.; Lewis, K.E.; Moore, J.W.; Goodrich, L.V.; Johnson, R.L.; Scott, M.P.;
Development 122, 2835-2846, 1996
A:Title: Spatial regulation of a zebrafish patched homologue reflects the roles of sonic
A:Reference number: Z18860; MUID:96379744; PMID:8787757
A:Accession: T18291
A>Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-1220 <CON>
A:Cross-references: UNIPROT:Q98864; EMBL:X98863; PIDN:CAA67386.1
C:Genetics:
A:Gene: ptc1
C:Superfamily: Drosophila membrane protein patched

Query Match 64.5%; Score 4042.5; DB 2; Length 1220;
Best Local Similarity 64.6%; Pred. No. 2.8e-272;
Matches 775; Conservative 156; Mismatches 224; Indels 44; Gaps 8;
QY 2 TRSP-----LRELPPSYTPPARTAQAIIAGSL---KAPLWIRAYFQGLLFLSLGCGIQ 52
DB 23 TRSPPPVNSDLRR--PSYC-HAFAALKQISGKAVGQKAPLWIRARFQAFLESLGCHIQ 79
QY 53 RHCKVFLGLLALGALALGLRMALITFNLFQWVEGSRVSOELHYTKELGEEAAVTS 112
DB 80 RHCKVFLGLLALGALALGLRMALITFNLFQWVEGSRVSOELHYTKELGEEAAVTS 139
QY 113 QMLQTRAQECENILTPREALGLHQAALTASKQVSLYKSWDLNKKICYKSGVPLIENGM 172
DB 140 QMLQTPKQEGTNILTQEAALLHLEALASAKVQVSLYKSWDLNKKICYKSGVPLIENVM 199
QY 173 IEWMIKFLPCVITLPLDPCFWEGAKLQGGSAIYLPGRPDIOWTNLDPEQLLBELGPFASLE 232
DB 200 IERMIDKLPFCMIVTLPDPCFWEGSKLQGGSAIYLPGRPDIOWTNLDPEQLLBELGPFASLE 259
QY 233 GFRELLDKAOGVAVGRPCPLHDDHCPSPANHHRSQAQPNVAHELGGCHGFSGKPMH 292
DB 260 GFREMLDKAOGVAVGRPCPLHDDHCPSPANHHRSQAQPNVAHELGGCHGFSGKPMH 319
QY 293 WQELLGGMARDPQCELLRAELAQSTFLMSPRLQYEHFRGDYQTHDIGWSEQAQSTVL 352
DB 320 WQELLGGERVKDSQNALQSAEALQTMFLMSPKQLYEHFKDDYEHIDINWNEKATAIL 379
QY 353 QAWQRRFVQLAQEALPENASQOIHAFSTTTDDIILHAFSEVSAARVGGYLLMLAYCVT 412
DB 380 ESQWQKFEVHVHGSTPQNSSNVVAFSTTTLNDIMKSPSDSVIRVAGGYLLMLAYCVT 439
QY 413 MLRWDCAQSGVGLGAVLLVALAVASGLGICALLGITNAATQVLPALAGIGVDDVFE 472
DB 440 MLRWDCAQSGVGLGAVLLVALAVASGLGICALLGITNAATQVLPALAGIGVDDVFE 499
QY 473 LLAHAFTALPGTLPQERMGECLQRTGTSVLTSTINMAAFMAALVPIPALRAFSLQAA 532
DB 500 LLGHSFTETRSNIPFKERTGDCLRGTGTSVLTSTINMAAFMAALVPIPALRAFSLQAA 559
QY 533 IVWGCTFVAVMLVPPAILSLDLRRRCORLDVLCFSPSCSAQVQIQLPQELGDT----- 586
DB 560 VVVWFENFAMALLIFPAILSLDLRRRCORLDVLCFSPSCSAQVQIQLPQELGDT----- 619
QY 587 -----GVPVGVIAHLTATVQAFTHCEASSQHVVTILPQAHL-VPPPS----- 628
DB 620 RAPATPTVTGTSITTTSTHTTTVQAFTHCEASSQHVVTILPQAHL-VPPPS----- 679
QY 629 --DPLGSELPFGSGSTRDLGQEEETROKAAKSLPCARWNLAHAFARYQAFAPLLQSHAK 686
DB 680 TTDPYGSQVFTTSSSTRDLGQEEETROKAAKSLPCARWNLAHAFARYQAFAPLLQSHAK 739
QY 687 AIVLVFGALLGLSLYGATLVODGALTDVVRPGTKEHAFSAQRYPSLYEVALVTQGG 746
DB 740 TVVVVVFVALLSLSLYGTMTWHDGLYLTIVPRDQVEYEFITAQFKYFSYNNVILVMDG 799
QY 747 FDYAHSQRALFDLHQRFSSLKAVLPPPTAQAPTQVLPALAGIGVDDVFLAHAPTE 806
DB 800 FDYAHSQRALFDLHQRFSSLKAVLPPPTAQAPTQVLPALAGIGVDDVFLAHAPTE 859
QY 807 RHSYRNGSEGDALAYKLLIOTGDAQEPLDFSQITTRKLVDRGLLPELFPYMGTLVWSS 866
DB 860 YDSYRNGSEGDALAYKLLIOTGDAQEPLDFSQITTRKLVDRGLLPELFPYMGTLVWSS 919
QY 867 DPLGLAASQANFYPPELWHLKDYTTGTLNLIIPPAQPLEFAQFPFLGLGLOKTDVFA 926
DB 920 DPLGLAASQANFYPPELWHLKDYTTGTLNLIIPPAQPLEFAQFPFLGLGLOKTDVFA 979
QY 927 IEGARAACAGVAVHVPSPGPFLEWQYGLGKLSAIPVILVAMTWELFGIMGLGKLSAIPV 986
DB 980 IEGARAACAGVAVHVPSPGPFLEWQYGLGKLSAIPVILVAMTWELFGIMGLGKLSAIPV 1039
QY 987 WTAGLIVLVAMTWELFGIMGLGKLSAIPVILVAMTWELFGIMGLGKLSAIPV 1046

Db 1040 WTAGVIVFIPMMVTVEFGIMGLIGIKLSAIPVIVILASVIGVETVHIALGFLTAIGD 1099
QY 1047 RNLRAHALEHTPAPYTDGNAISTLLGLMLAGSHFPIVRYPPAALTIVTLGLLHGLVL 1106
Db 1100 RNTRSVAMEHPAPVIDGAISTLLGLVLAGSEDFIMRYFFAVLAITLLGILGLVL 1159
QY 1107 LPVLLSILGPPPEVI-----QWKSPSPEILSPAPQGGGLRWGASSLPQSPARVTT 1159
Db 1160 LPVLLSLMGPPAEVVPANNANHLQSPSPMPMPNMHHGYAGHIPKASHQAFSETSDS 1218

RESULT 3
Ti8538
patched protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18538
R:Marigo, V.; Scott, M.P.; Johnson, R.L.; Goodrich, L.V.; Tabin, C.
Development 122, 1225-1233, 1996
A:Title: Conservation in hedgehog signaling: induction of a chicken patched homolog by S
A:Reference number: Z18958; MUID:96205046; PMID:8620849
A:Accession: T18538
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1442 <MAR>
A:Cross-references: UNIPROT:Q90693; EMBL:U40074; NID:g1335850; PID:g1335851; PIDN:AAC598
C:Genetics:
A:Gene: PTC
C:Superfamily: Drosophila membrane protein patched
C:Keywords: transmembrane protein

Query Match 53.3%; Score 3340; DB 2; Length 1442;
Best Local Similarity 54.3%; Pred. No. 2.1e-223;
Matches 663; Conservative 204; Mismatches 304; Indels 50; Gaps 17;

QY 12 PSYTPPARTAAPQIILAG---SLKAPLWLRAYPQGLLSIGCGIQRHCGKVLPLGLLAFGA 68
Db 54 PSYC-DAFALEQIAKGRATGRAPLMURAKEQRLLENLGCYIQKCGKFLVWGLL-YSA 111
QY 69 LALGRMAIETNLBOLWVEGSRVSOELHYKELGEEAAVTSQMLIQARQEGENILT 128
Db 112 FAVGLRAANLETNBELWVEGSRVSRLENTYQKIGEEAFNPQMLIQTPQEDGTNVL 171
QY 129 PEALGLHLOALTASKQVSVLYGKSWDLNKLCKYSGVPLIENGMEWIEKLPFCVILT 188
Db 172 TEALRQHLDSALQASRVHYMYNRMWKLEHCYSGSELTIEAGYMDQIIEYLYPCLITP 231
QY 189 LDCFWEKAKLOGGAYLFGRPDIQWNLDPQELLEELGPF-ASLEGFRELLDKAQVQAY 247
Db 232 LDCFWEKAKLOGGAYLGLKPLQWLNFDPLFLEELKKINYQVESWEEMLNKAEVGHY 291
QY 248 VGRCLHPDDLHCPSPANHHRSQAPNVABELSGCGHGFHKFMHQBELLLGGWARDPQ 307
Db 292 MDRPCLNPADPCITAFENKNSKTPDLVALVSGCYGLSRKYMHWQBELIIGGTVKNS 351
QY 308 GELLRAEALQTELLMSRPLYEHPRG-DYQTHDIGSEEOASTVLAQWRFFVOLAQEA 366
Db 352 GKLVSAQALQTFQMLTPQMYEHFKGYEYVSH-INNNEDKAAALEAWQRMYYEVVHQ 410
QY 367 LPENASQOIHAFFSTTDLILHAFSEVSAARVWGGYLLMLAYACVTMLRWDCASQGSVG 426
Db 411 VAQNSTQKVLSTTTTLDLILKSDSVIRVAGSYLLMLAYACVTMLRWDCASQGSVG 470
QY 427 LAGVLLVALAVASGLGICALGIFTNAATTQVLPFLALIGVDVDFLIAHAFTALPG-- 484
Db 471 LAGVLLVALSVAAGLGLCSLIGSFNAATTQVLPFLALGVGVDDVFLLAHAFSETGNKR 530
QY 485 TPLQRMGECLQRTGTSVLTSTINMAAFMLAALVPALRAFSLOAAIVVCGTFVAVML 544
Db 531 IPFEDRTGECUKRTGASVLTSTINVTAFMAALIPALRAFSLOAAIVVVFVAVML 590
QY 545 VFPAILSLDLRRRQRDLVLCFSSPCSQAQVIQILPQLGDI-----GTPVGVIAH--- 595

Db 591 IFFAILUSDLYRREDRRLDIFCCFTSPCVTRVIOIEPQAYEAENDNICSSPPYSSHFA 650
QY 596 -----LTATQAFTHCEASSQHVVTILPPQAHLVPPP-----SDPLGSLFSPGGSTRDL 645
Db 651 HETQITMQSTVQLRTYEDPHTQAYYTTAEPRSEISQVQVTVTQDSLSCQSPESASTRDL 710
QY 646 LQOEETROKAAACKSLPCARWNLAHFARYQFAPLQLQSHAKAIVLVLFGLGLGLSLYGAT 705
Db 711 LSQFSDS--SVHCLPEPPCTKWTLSLTPAEKHAFPLLKPKAKVVVIFELGLGLGLSLYGT 768
QY 706 LYQDGLALTDVVPRTGKHEAFLSAQLRYSLEVALVTGGFDYAHSAQRALFDLHORFSS 765
Db 769 RVRDGLDLTDIVPDRTRYDFIAAQFKYFSYNNMIVTQKA-DYPNVQHLHLEHRSFSN 827
QY 766 LKAVLPPPATQAPRTWLYHRYRNWLGIOAAFPQDQWASGRITRHSYRNGSEDGALAYKLLI 825
Db 828 VTYVLEGGDROLPKWMLHYFRDMLQGLQDAFDSQWETGKITYSYKNGSDDDAVLAAYKLLV 887
QY 826 QTGDAQEPLDFSLQTRKLVDRGLIPPELFWMLTVMVSSDPLGLAASQANFYPPPEW 885
Db 888 QTGNRAKPIDISQLTKRVLVDADGIINPNAFYIYLTAWVSNDPVAYAAASQANIRPHREW 947
QY 886 LHDKYDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADPVEALEGARAACAAGAGVHA 944
Db 948 VHDKADYMPETRLRIPAAEPIEYQFPFYNLGRLRETSDFVEAIEKVRACNNYTSLGAS 1007
QY 945 YPSGSPFLFWEOYLGLRRCFFLIAVCIILVCTPLVCAILLNPWTAGLIVLVLMVMTVELF 1004
Db 1008 YNGYPFLFWEOYIGLRHWWLLSISVVLACFLVCAFLFNWPTAGIIVVUVALMTVELF 1067
QY 1005 GIMPLGLKLSAIPVIVILVASVIGVEFTVHVALGFLTQGSRNLRRAHALEHTFAPVTD 1064
Db 1068 GMMGLIGIKLSAIPVIVILASVIGVEFTVHIALAFLTAIGDKNRRAVLALEHMFAPVLD 1127
QY 1065 GAISTLLGLMLAGSHDFIVRYPPAALTIVTLGLLHGLVLLPVLSILGPPPEVI--- 1121
Db 1128 GAVSTLLGVLMAGSEDFIVRYPPAVLAITLLGVNLGLVLLPVLSFFGFPYEVSPAC 1187
QY 1122 ---QWKSPSPEILSPPA-----PQGGGLRWGASSLPQSPARVTTMTVAIH---PPPL 1169
Db 1188 GRNRLPTSPS-PPPSIVRFALPFGHTNNGSDSDSYSSQTVTSIGISELHLYEATQS 1245
QY 1170 PGAYIHAPDDEPPSPATSS 1190
Db 1246 PGIFVHVQVVEATENPVFARS 1266

RESULT 4
T30172
transmembrane protein patched - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30172
R:Goodrich, L.V.; Johnson, R.L.; Milenkovic, L.; McMahon, J.A.; Scott, M.P.
Genes Dev. 10, 301-312, 1996
A:Title: Conservation of the hedgehog/patched signaling pathway from flies to mice: indu
A:Reference number: Z20752; MUID:96176226; PMID:8595881
A:Accession: T30172
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1434 <GOO>
A:Cross-references: UNIPROT:Q61115; EMBL:U46155; NID:g1181884; PID:g1181885; PIDN:AAC987
A:Experimental source: clone M2, M9
C:Superfamily: Drosophila membrane protein patched

Query Match 53.2%; Score 3337; DB 2; Length 1434;
Best Local Similarity 53.1%; Pred. No. 3.4e-223;
Matches 672; Conservative 206; Mismatches 309; Indels 78; Gaps 20;

QY 3 RSPPLREL--PPSYTPPARTAAPQIILAGSL---KAPLWLRAYFQGLLSIGCGIQRHCGK 57
Db 28 RAAPDRDYLHRPSYC-DAFALEQISKGKATGRKAPLWLRAKEFORLLFKLGICYIQKCGK 86

Db 214 EGSQLLGPESAVVPCINQLRLWTLINPASVMQYMKQKMSBEKISF-DFETVEQYMKRAA 272
 QY 243 VQAYVGRCLHPDDLHCPSPNHSRQAPNVVAHELSGGCHGFSKFMHWOBEILLQGM 302
 Db 273 TASGYNKPCPLNPNCPDTPNKNSTOPPDVGAILSGGCYGYAAKHMHPPEELIVGGA 332
 QY 303 ARDPQGLLRAEALSTFLLMSPROLYEHFRGDYDTHDYGWSEBOASTVLQAWORRFVQL 362
 Db 333 KNRSHGLRKAALQSVQLMTEKEMYDQWQNYKVHHLGWTQEKRAAEVLNWAQRNFSRE 392
 QY 363 AQEALPENAAAAQIHAFSSTLDDILHAFSEVSAARVGGYLLMLAYACVTMLRW-D 417
 Db 393 VEQLLRKOSRIATNYDIYVFSSAALDDILAKESHPALSIVIGVAVTVLYAFCTLLWRD 452
 QY 418 CAQSGSVGLAGVILVALAVASGLGALLGTENAAATVQLPFLALGIGVDVDFLLAHA 477
 Db 453 FVRGSSVGVAGVLLMCFSTAAGLGLSALLGIVFNAASTQVVPFLALGIGVDVDFLLAHA 512
 QY 478 FTEALPGTLPQRMGECIQTGTSTVLTSLNNMAAFMAALVPIPALRAFSLQAAIVVGC 537
 Db 513 YAE-----SNRRQTKLLKKGPSILFSACSTAGSFFAAAFIPVPAKVCLOAAIWMCS 568
 QY 538 TFVAVMLVFPALSLDLRRRHQRDLVLCFSSPSCSAQ---VQILPOELGSDGTVPVGTA 594
 Db 569 NLAAALLVFPAMISLDLRRRTAGRADIFCCCPVWKEQPKVAPPVPLNNNG----- 621
 QY 595 HLTATVQAFTHCEASSQHVVTILPQAHLVPPSPDLGSELSPSGSGSTRDLGQBEETRQ 654
 Db 622 -----RGARHPKSCNNRVAL-----PAONPLEQORADIPGSSHSL----- 657
 QY 655 KAAKSLPCARNLAHAFARYOFAPLLQSHAKAIIVLFLGALLGLSLYGATLVQDGLALT 714
 Db 658 -----ASESLATFAHQYTPFLMRSWKFLTWGFLAALISLSTASTRLQGLDII 708
 QY 715 DVVPRGTKEHAFSLAQRYSLYELVALVTQGFYAHSQRALFDLHQRFSSILKAVLPPPA 774
 Db 709 DLVPKDSNEHKFLDAQTRFLGFYSYAVTQGNFXYPTQQLRDYHDSFVRVPHVKNDN 768
 QY 775 TQAPRTWLYHYNNMLOGTQAFDQDQWASGRITRHS-YNGSEDGALAYKLLIQTGDAQEP 833
 Db 769 GGLPDLFWLLLFSEMLGNLQKIFDEYRGRITKECFNFENASSDAFLAYKLIVQTHVDNP 828
 QY 834 LDFSQLTRKLVDRGELIPPELFYVGLTVWV-SSDPLGL-----AASQANFYP 880
 Db 829 VDKEVLVTLNRLVNSDGIINQAFYNLSAWATNASSPTELIRANCIRNANGASGKLYP 888
 QY 881 PPPWLH--DKYDTGENLRIPPAQLEFAQFPFLRLGLQKTAQDFVEAIEGARACABAG 938
 Db 889 EPROYFHQPNED-----LKIPKSLPLVYAQMPFYLHGLTDTSOIKTLIGHIRDLVKYE 943
 QY 939 QAGVHAYPSGSPFLFWEOYGLRRCF-LLAVALIVCTFLVCALLNPWTAGLIVLVA 997
 Db 944 GFGPNVPSGPPFIFWEQYMLRSLAMLACVILLAAVLV-SLLLSVMAAVLIVLSVL 1002
 QY 998 MMTVELFGIMGFLGKLSAIPWVILVASVIGVBFTVHVALGFLTTQGSRLRAAHLEH 1057
 Db 1003 ASLAQIFGAMTLLGKLSAIPAVILLSVGMMLCFNVLSIGFTSVGNRRVQLSNQM 1062
 QY 1058 TFAVTDGAISTLGLMLAGSHDFIVRYFAALTVLTLGLHLGLVLLPVLVLSILGPP 1117
 Db 1063 SLGPLVHGLMTSGVAVFMLSTSPFEFVIRHFCWLLLVLCVGCACNSLLVFPILLSMVGPE 1122
 QY 1118 PEVLQMYKESPEILSPAP 1136
 Db 1123 AELVFL--EHPDRISTPSP 1139

RESULT 6

T27969

hypothetical protein ZK675.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T27969

R.Sims, M.
 submitted to the EMBL Data Library, November 1994
 A:Reference number: Z20448
 A:Accession: T27969
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1405 <WIL>
 A:Cross-references: UNIPROT:009614; EMBL:Z46812; PIDN:CAA86843.1; GSPDB:GN00020; CESP:ZK
 A:Experimental source: clone ZK675
 C:Genetics:
 A:Gene: CESP:ZK675.1
 A:Map position: 2
 A:Introns: 31/1; 59/3; 100/3; 244/2; 485/1; 950/2; 1298/2; 1335/3
 C:Superfamily: Drosophila membrane protein patched

Query Match 27.2%; Score 1708.5; DB 2; Length 1405;
 Best Local Similarity 31.5%; Pred. No. 3.8e-110;
 Matches 433; Conservative 203; Mismatches 440; Indels 299; Gaps 31;

QY 34 LWRAYFGCLLPSLGGCQIRHCGKVFLGLAFLGALALGLRMAIETNLQWLVEVSGRV 93
 Db 110 LYSRLIQKLLFALGNTVHRNAWSIILAVSMIFAVCCYGLQVHIETDIVKLVAQGGRL 169
 QY 94 SOELHY---TKEKL-----GEBAAYTS-----OMLIQTARQGENILTPALGLHLQ 137
 Db 170 DEELNLFENIKEAMNVTGDSGPPELFRENGGLGGYQVLIQTPEYEGDALAAGPLLKHEV 229
 QY 138 AALTASKVQVSLYKSWDLNKICVKGVPPLI-----ENGMIEMWIKLPCCVILTLPDCCFW 193
 Db 230 IMKHIAFNVSVHGVDSLSLDCFKPAPPSVAADSAASLGDVIDKIVPCITWITDPCFW 289
 QY 194 EGAKLQGSAYLP-----GRPIQWNLDPQLLEELGFFASLEGFREL 238
 Db 290 EGSKALGPHPLPKSSSLGPLGMLSSLSLSDGMIRWSDFPIAVIDEIHRSFNLSGHTFF 349
 QY 239 DKAQVQAYVGRPCLLHDPDLHCPBSAPNH----- 267
 Db 350 ERAGVSHGYMDRPCIDPLDPECPWAKNYFDCPHIDRVRIAKKYGTELEEEKKDSGY 409
 QY 268 -----HSRQA---PNVAH----- 277
 Db 410 SFFDFLGRKKEAGDOPKMIHPAQADSIPTIEDAVPAQVPVSTAPIPTTTTILSPPEARA 469
 QY 278 ----- 285
 Db 470 AEEKEKKQARELKDYCKSYKSAFEMLKKNKDKWPEVMSNNYPQNVDAEMTGGCGS 529
 QY 286 FSHKFMHWEELLGGWARDPQ-CELLRAEALQSTFLLMSPROLYEHP-----RGDYOTH 339
 Db 530 FASNVLWPEMDILGNPRKAKGKLSGADALQSVFLVSPADVFLPKQPKGRNSMKTG 589
 QY 340 -DI-GWSEEQASTVLQAWRRFVQ-----LAQEALPENASQOIHAFFSTTLDIIHAFSE 392
 Db 590 LMDAMNETAAEQVLQAWQRNFTKSLYNHKNANVDGDNERRTLHPLASTSIADMLEFCQ 649
 QY 393 VSAARVVGYLMLAYACVTMLRW-----CAQSGSVGLAGVILVALAVASGLGALLG 448
 Db 650 FNYTIILAGVLMAYAIQVQARFDCNCLPATESPMSGLALAGLVVTVFASVAGLGLATWFG 709
 QY 449 ITENAAATVQLPFLALGIGVDVDFLLAHATEALPGTFLQRMGECIQTGTSTVLTSLIN 508
 Db 710 IEFNAATQIVPFLTIGLIGVNDPMFLHNYRDVVVKLAGHAEMLMRETMGSILCTSLIN 769
 QY 509 NMAAFLMAALVPIPALRAFSLQAAIVVGCITFVAVMLVFPALSLDLRRRHQRDLVLCCE 568
 Db 770 NILSFLTGTLPIPALRSFCAQSILLTFNFIALITYPAIISIDLRRKKAQRDLVCCCL 829
 QY 569 SSPCSAQVIOILPOELGSDGTVPVGIAHLTATVQAFTHCEASSQHVVTILPQAHLVPPPS 628
 Db 830 -----YGD-----TREESYS-----MISKPK 845
 QY 629 DPLGSELSPGSGSTRDLGQBEETRQKAAKCSLPCARNLAHAFARYOFAPLLQSHAKAI 686

354 IIPFLAFITVCSSGLVFLVQVTTNPVELMSAPHSQARLEKEYFDKHF--PPFRTBQLII 411
118 TARQEGENILTPALG-----LHQAALTASKVOVSLYGKSWDLNKIC 160
412 QAPNTSVHIYEPYAGADVFPGLPKNKEILHQLVNLQIAI--ESITASYNNETVTLQDIC 469
161 YKSGVPLIENGMEIWMIEKLPFCVILTPLDCFEWAKLOGGSAYLPGRPDIQWNTLNDPEQ 220
470 VAPLSFYKNK-----CTINSVLNYP-----QNSHRAVL----- 496
221 LLEELGPFASLEGFRELDDKAQVQYVGRPCLLHPDDLHC--PPSAPNHSRQAPNVAHE 278
497 -----DSQVGDDFYIYADVHTFLYCVRAPASLNDTSL----- 529
279 LSGGCHG-FSHKFMHQBELLLGGWARDPOGELLRAELQSTFLMSPRLYEHFRGDYQ 337
530 LHGPCLGTFGGVPFW--LVJGGY--DDQ--NYYNATALVITFPV-----NYYNNDTE 576
338 THDIGWSEEQASTVLQAMORRVQLAQEALPENASQOIHAFSSTLDDILHAFSEVSAAR 397
577 RLQRAW-----AWEKEFISFVKVY--KNPNLTISFTAESIEDELNRESNDVPT 624
398 VYGGVLLMAY-----ACVTMLRWCDAQSQSGVGLAGVLLVALAVASGLGLCALIG 448
625 VLIISYVVMFLYISLALGHITQSCRLL-----VDSKISLGIAGILIVLSSVACSLGIFSYMG 680
449 ITFNAATTQVLPFLALGIGVDVDFLLAHAF--TEALPGTFLQERMGECLQRTGTSVWLTS 506
681 MPLTLIVIEVLPFLVLAGVDNIFILVQTYORDEQLQEBETLQQQGRILGEVAPTFWFLSS 740
507 INNMAAFMAALVPIPALRAFSLQAAIVVCGTCFVAVMLVFPAILSLDLRRHRCQLDVLIC 566
741 FSETSAFFGALSSMPAVHTSLFAGMVLIDFLQITCFVSLGLDGRKQKNHLDLIC 800
567 CFSPSCSAQVIOILPQELGDGFPVPGIAHLTATVQAFTHCEASSQHVVTILPPOAHLVPP 626
801 C-----VRGADDGQGS-----HASESY----- 817
627 PSDPLGSELSPFGGSTRDLLGOEBETRQKAACKSLPCARWNLAHFARYQAPALLQSHAK 686
818 -----LPRFFKNYFAPLLKDWLR 836
687 AIVLVFGALLGLSLYGATLVQDGLALTDVVPGRGTHKHAFLSAQLRYFSLY-----EVAL 741
837 PIWAVFVGLVSFAVNVKVDIIGLQSLNP-----NDSYVIANFKSLAQVILHSGPPYVF 892
742 VTQGFDA--HSQALFD-----LHQRFFSLKAVLPPPPATQAPRTWLHYRNWLQ 790
893 VLEEGYNSRRKQGMVCGMGCONDSLVOQIFNAAEELDTVTVGVFAPSSWIDDYFDWVS 952
791 GIQAADFQDMSAGRI--TRHSYRNGSEDGALAYKLLIQTGDAQEPLDPSQLTTRKLVDRE 848
953 PQSSCC-----RLYNVTHQFCNAS-----VMDPTCVRCRPLTP-E 986
849 GLIPPE--LFTVGLTVMVSSDPLGLAASQANFYPPPPPEWLHDKY-----DTTGENLRIPPA 902
987 GKQEPQGEKFKLPMFLSDNP-----NPKCKGGAHAGSANNVIGDITYIGAT 1036
903 QPLEFAQFPFLRLGLQKTADPVEAIEGRARACABAGQ-----AGVHAYPSGSPFLFEWQ 956
1037 YFMTYHTI-----LKTSDYTDAMKARLIASNITETMRSGSDYRVFFPSYVFVFFEQ 1090
957 YLGRRCFLLAVALCILLVCTELVACALL--LNPWTAGLVVLVAMTVELFGIMGLFKLS 1015
1091 YLTIIDDTFNLVSLGSIPLVTLVWGLCELMASAVIMCITAMILVNMFGVMWMLGISLN 1150
1016 AIPVVILVASGIGVEFTVHVALGF-LTQGSRLNRAHAHLHTFAPVTDCAITLL-GL 1073
1151 AVSLVNLVMSGSISEVFCSHITRAFTMTSGSRVSRABEALAHMGSSVFSGITITKFGGI 1210
1074 LMLAGSHDFIVRYFFFAALTATVLLGLLGHVLLVPLLSILGP 1116
1211 VVLAFAKSQIEIFEFYFRMYLAMVLLGATHGLIFLPLVLLSYIGP 1253

RESULT 9

T05663

hypothetical protein F22113.120 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T05663

R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15420

A:Accession: T05663

A:Molecule type: DNA

A:Residues: 1-1055 <BEV>

A:Cross-references: UNIPROT:Q9SVF0; EMBL:AL035539

A:Experimental source: cultivar Columbia; BAC clone F22113

C:Genetics:

A:Map position: 4

A:Introns: 24/3; 60/3; 99/3; 150/1; 193/1; 216/3; 278/3; 297/2; 336/3; 364/3; 396/3; 419/26/3

A:Note: F22113.120

Query Match

Best Local Similarity 8.2%; Score 514; DB 2; Length 1055;

Matches 238; Conservative 137; Mismatches 328; Indels 424; Gaps 35;

QY 36 LRAYPQGLLFLSGCGIORHCGKVLFLGLLAFGALALGRMAITNLEQLWVEVGSRSVQ 95

DB 288 VQRYMAKFRSVSGSWIARNPSILVFMVAIVLALCSGLYNFKVETRPKLVGPESKAAE 347

QY 96 ELHYTEKLGEEAAYTSQMLTQTAQE-----GENILTEALGLHLQAALTASKVQVSLY 150

DB 348 EKKFFDTHL--SPFYRIEQLILATVPDKSGRAPSIIVTDENIL----- 389

QY 151 GKSWDLNLCYK-----SGVPLIENGMIENMIEXLFCVILTPLDCFWEGAKLOGG 201

DB 390 --LFDIQKYFMDSGTDFDYGGVEHAYCYQHYTSSETCLSAFOAPVD--PSAVLGGF 444

QY 202 SAYLPGRPDIQWNTLDPQLLEELGFPASLEGFRELDDKAQVQYVGRPCCLHPDDLHCP 261

DB 445 SG-----NNYSEVMVSELG-----CSVPFD----- 464

QY 262 PSAPNHSRQAPNVNAHELSGGCHGFHKFMHWQBELLLGGWARDPQGBELLRAELQSTFL 321

DB 465 -----CYS-----DVKRTLFQATAFVVTYP 484

QY 322 LMSPRQLYHEPRGDYQTHDIGWSEEQASTVLQAMORRVQLA-GEALPENASQOIH-AFS 379

DB 485 V-----NVVIGDS-----SNENARAV--AWEKSFQIAKEBELLPWVRSKNLSUSFS 528

QY 380 S-TTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ-----SQGSVGLAGVL 431

DB 529 SESSIEBELKRESTDVITTAASVLMFVYISVTL--GDAPQFYTFYISSKVLGLSGVV 586

QY 432 LVVALVASGLCLCALLGITFNAATQVLPFLALGIGVDVDFLLAHAFTEALPGTFLQERM 491

DB 587 LVLLSVLGSVGVSFALGVKSTLIIMEVLPFLAVGVGDNMCLLVHAKVROPREVSLEQRI 646

QY 492 GECLQRTGTSVWLTSINNMAAFMAALVPIPALRAFSLQAAIVVCGTCFVAVMLVFPALLS 551

DB 647 SSALVEVGPSITLASLSEVLAFAVGFPMFPACRFISMFAALIMLDFFTQITAFVALIV 706

QY 552 LDIRRHRCQBLDVLCCFSPSCSAQVIOILPQELGDGTVVPVGVIAHLTATVQAFTHCEASSQ 611

DB 707 FDCKRSADNRIDCFPCIKVFPSS-----RESVEG----- 735

QY 612 HVVTILPQAHVPPSPDPLGSELPFGGSTRDLLGOEBETRQKAACKSLPCARWNLAHF 671

DB 736 -----GRE-----PG-----FLERY 745

QY 672 ARYQFAPLLIQSHAKATVILVFGALLGLSLYGATLVQDGLALTDVDPGRGTHKHAFLSAQL 731

DB 746 MKEVHAPVLGLMGVGMVVAVVFA-----FALASIIISRASQ----- 781

QY 732 RYFSLYEVALVTGGFDYAHSORALFDLHQRPFSSLKAVLPBPATQAPRTWLHYRNWLOG 791
DB 782 -----ASDTSYIAKPAA-----SWLD- 797
QY 792 IQAAFDQDASGRITRHSYRNGSEGDALAYKLLIQTGAQBPFLDFSQLTTRKLVDRGLI 851
DB 798 -----DF----- 799
QY 852 PPELFYMGITVWSSDPLGLAASQAN-FYPPPPPEWLHKYDTGTGNLRIPPAQPLEFAQF 910
DB 800 -----LWMLSPEAFGCCKEFTNGSVCPDDCCFRHSDLVOD--RPSTAQPRE--KL 846
QY 911 PFLRLGLQKTADFEA-----IEGARAAACAEAGQ-----AGWYAYPSGSPFF 951
DB 847 PWFNLAL-PSADCAKGGHAYTNSVDLKGYESGVIOASEFRTHYPTLNTQIDIFFYSVFY 905
QY 952 LFWEQYGLRRCFLAVCILLVCTFLVCALLILNPTAGLIVLVLAMTVELFGIMGFLG 1011
DB 906 IFFEQY-----LNWTVALTNLALAI-----VG 928
QY 1012 IKLSAIPVILVASGIGVEFVHVVALGFLTTQGSRNLRRAHALEHTFAPVTDG-AISTL 1070
DB 929 IQLNAVSVVNLIMSIGIAVEFCVHI SHAPLMSGSDREHRAAREALETMGASVFGITLTKL 988
QY 1071 LGLMLAGSHDFIVRYEFAALTVLTLGLLHGLVLLPVLSILGPP 1117
DB 989 VGVIVLCFARSEIFVYVYFQMYLALVITGLFHLGLVFLPVILSLAGPP 1035

RESULT 10
T21612
Hypothetical protein F31F6.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21612
R:Percy, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19449
A:Accession: T21612
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-955 <WIL>
A:Cross-references: UNIPROT:Q19945; EMBL:Z69884; PIDN:CAA93751.1; GSPDB:GN00028; CESP:F31F6
A:Experimental source: clone F31F6
C:Genetics:
A:Gene: CESP:F31F6.5
A:Map position: X
A:Introns: 64/2; 141/3; 255/3; 308/1; 409/1; 435/3; 484/2; 579/1; 632/2; 715/3; 777/3; 8

Query Match 7.4%; Score 465.5; DB 2; Length 955;
Best Local Similarity 21.2%; Pred. No. 4.5e-24;
Matches 230; Conservative 176; Mismatches 414; Indels 267; Gaps 45;

QY 166 PLIENGMIW-----MIKLF-----PCVILTPLDCEWE 194
DB 8 PLVRNA-FEWYGPVVRWVWFCEISFLTLACSVGFRMTLRVDVDPVYVTFPSDARW- 65
QY 195 GAKLOGGSAYLPGRPDIOWTN-----LDPEQLLEELGPFASLEG--FREILLDKAQVQAVY 248
DB 66 -----RREISVFENWVLDENKFL-----PGKSFEAKRFRVNLIRAKDGGSIM 108
QY 249 GRPCLH-----PDDLH-----CPPSAPHNH-----SRQA 272
DB 109 RDNVLHEIRINQWIMNNTSIPTDDLKFNLTVDCLCLSYDWC---GANEHIQMLRRND 165
QY 273 ENVAHEL---SGCGHGFHKFMHWQELLIGGNARDPQ---GELLRAEALQSTFLIMSP 325
DB 166 VNOILDLHFRGGTK-----DTPVYLGIGFQVDFQNGTQSDAKLTQLFYELKQD 216
QY 326 RQLYEHFRGDYQTHIGWSEEQASTVLQAWQRVQLAQBALPENASQOIHAFSSTLDD 385
DB 217 QKMVEEYSSKFSVALETFLNQVYSSDVITLSFAHYQSLEDGLDENAK---AF-----VFN 268

QY 386 ILHAFSEVSAARVYGGYLLMLAYACVTMLRWDCAQSGSVGLAGVLLVALAVASGLGLCA 445
DB 269 FVVSFFVLMYALVSSFTLKSSSA--TKIDW--ISSKEFWLAAGMFSIVLSIISAFGLF 324
QY 446 LLGITFNAATTQVLVFLALG-----IGVDDVFLLAHAATEALPGTFLQER 490
DB 325 ILGVRYNVINT-IIPFLIIGBFQSFKNMEKQKIIPAIGIDDMFLMNACWDQTSKLSVPER 383
QY 491 MGECLQRTGTSVLTSTINMAAFMAALVPALRAFSLQAAIVGCTFVAVMLVFPAIL 550
DB 384 MSKTLSHAGVAVTITNVDVMSFAIGCTIDLPQGFCCYACVSFAFSFYQLTTFSSGAM 443
QY 551 SL-----DLRRHC-----ORLDVLCFSPSCSAQVIQILPOELGDGTVPVGIHAHLAT 599
DB 444 AIMGEVEREKHCLFFYRTFOVDI-----SKMNEEADSKLQIKRSASPAFNYLSS 498
QY 600 VQAFTHCEASSQHVVTILPQOHLVPPSPDPLGSELFSFGGSTRDLLQOEETROKAACK 659
DB 499 NSSFSDDSDSFSSKXTI-----PAEPFAWKEQSQSPNSS-----LSKKSXDREB--- 540
QY 660 SLPCARNWLAHFARYQFAPALLQSHAKAIVLVLFGALLGLSLYGATLQDGLALTDVVER 719
DB 541 -----KDRIVHFHIGKIYGFILNSVRIFSGLIFVYLAIAWYGCYNFREGLNPNGLV-- 593
QY 720 GTKBHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHQRFSLSKAVLPPPTQAPR 779
DB 594 -TNDHYI-----AKYFS-----DIKHFWIGAGLH-----VAVLNP-----PN 625
QY 780 TWLHYRNWLOGIQAAFDQ-DWASGRITRHSYRNGSEGDALAYKLLIQTGAQBPFLDFSQ 838
DB 626 LTISENRNELLKVSASFENTQVTLGR-----EGTVPFLL-----EVLNLS 666
QY 839 LTRKLVDRGLIPPEL-----FYGLTVWYSS-----DPLGLAASQANFYPPPP 883
DB 667 ELNAEVEDTERLWKTKLNSWLKYTGSTQWASNLKINKITDGSFQAFRQIAUKNFVEP-- 724
QY 884 EWLHDKYDTGTGNLR-IPPAQPLEFAQFPFLRLGLQKTA-DFVEAIEGARAAACAEAGQAG 941
DB 725 -----NDHKHAQALLRDIAHQDFNVVHVHVSFGNRKILNDFISS-----HSCYAKKNIP 775
QY 942 VHAYPSGSPFLFWEQYGLRRCFLLAACILLVCTFLVCALLILNPTAGLIVLV-LAMMT 1000
DB 776 KLAFF-----FADQYLIILPATIQNVVISLILC-MAVVSFLLVPSLPSGFFVFSIVSIN 828
QY 1001 VELFGIMGFLGILKLSAIPVILVASGIGVEFVHVVALGFLTTQGSRNLRRAHALEHTFA 1060
DB 829 IGVFGYMTLWGNLDVAVSMISIIIMSIGFAVDLSAHTIYAFVTSHGDTKORVIGALETLGW 888
QY 1061 PVTGCAISTLLGLMLAGSHDFIVRYEFAALTVLTLGLLHGLVLLPVLSILSGPPEV 1120
DB 889 PIFQASSTIAGISILY-TVDAYIILVFPKTIWLTMLIGAIHGLFPFIPFLSLF--PVFE 945
QY 1121 IQMYKES 1127
DB 946 FRIPKSS 952

RESULT 11
T25600
Hypothetical protein C32E8.8 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25600
R:Gatung, S.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of *C. elegans* cosmid C32E8.
A:Reference number: Z20056
A:Accession: T25600
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-933 <GAT>
A:Cross-references: UNIPROT:P91129; EMBL:U88308; PIDN:AAB42325.1; GSPDB:GN00019; CESP:C3

A: Experimental source: strain Bristol N2; clone C32E8

C: Genetics:

A: Gene: CESP: C32E8.8

A: Map position: 1

A: Introns: 145/1; 177/2; 385/1; 418/3; 833/3; 878/3

```
Query Match          7.1%; Score 444; DB 2; Length 933;
Best Local Similarity 21.4%; Pred. No. 1.4e-22;
Matches 217; Conservative 170; Mismatches 398; Indels 228; Gaps 37;

QY 204 YLPGRP-----DIQWNL--DPQLLEELGPFASLEGFRELIDKAQV---GQAYVGRP-C 252
DB 81 YIPGRAVTSQBETQVLTALARNDSNILDKPFANAVYQLDKYIQTRVVLHNGHYYSYKNC 140

QY 253 LHDDDLHCPSPAPNHSRQAPNAHSLGSGCGF--SHKFMWQEBELLGGHWARDPQGL 310
DB 141 LQYKNGGCSNKHVHLSLHN-----HGFNITYPYFRFGSE---GGYIGSSLGV 188

QY 311 LRABALQSTFLMSPRLYEHFRGDYQTHDIGWSEBQASTVLQAWORRFVQLAQEALPEN 370
DB 189 TWKMGENTDILASAKAM-----FMVYHAKFHPBEMSYISGEWELEGRMLTQ-YPED 240

QY 371 ASQIHAFSTTLLDILHAFSEVSAARVGVGVLMLAYACVTMLRW-----DCAQSOG 423
DB 241 PYISITYFHSQTLADELKENADTLIPRFIISITLLIVFSTLCSLSPIDGFSFSDWLSKP 300

QY 424 SVGLAGVLLVALAVASGLGLCALGIGTENAATVLPALGIGVDVDFLLAHAFTEALP 483
DB 301 ILSILGVVSAGAILTGVFLSMGPYN-DIVGNVPLVLAGVDNMFELMAVAARRTSR 359

QY 484 GTPLOEGECLORTGTSVVLTSINMAAFMAALVPIPALRAFSLQAAIVVGCTFVAMV 543
DB 360 THTVHERMGECLADAASVILITSDVLSFGVGAITTPAVGICVYTGVAIFPAFIYQI 419

QY 544 LVFPALSLDLRRRCORLDVLCFSSPCSAQVQILPQELGD-GTVPGVIAHLTATVQA 602
DB 420 TFFAACALAMKHEASGRNSLFLIEAVSAEKKTSLSLTFORLNLGSPV-----467

QY 603 FTHCASSOHVVTILPPQAHVLPSPDPLGSELPFGSGSTRDLLQBEETROKAAKSLP 662
DB 468 ----DHSASHV-----KQPLTSRFF-----484

QY 663 CARWNLAFARYQFAPLLQSHAKAIVLVFGA-LLGLSLYGATLVQDGLALTDVVRGT 721
DB 485 -GEW-----YAPVLMHPVVRGIAMVWFVYLLGAS-YGCSRIKGLGEPNVLVDS 533

QY 722 KEHAFSLQALRYFSLY--EVALVTGGEDYAHSQRALFDLHQRFSLKAVLPPPPATQAPR 779
DB 534 YAIPIHYRLLEKRYFKYGOQVQVINNAPDLRN-----HTRDRVRHAMVLDPATSKHA 585

QY 780 TWLHYRNWLQIOAAAPQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQ 839
DB 586 IGMESVQFWLFEMERYOKELEVQIIDSFY-----GLLHHFLASKT-----627

QY 840 TTRKLVDREGLIPPELFYMGTLVWVSDPLGLAASQANFYPPPELWHDKYDTTGENLRI 899
DB 628 -----NNPL-----AEDIYWGMPD-----DDNGTWVK- 650

QY 900 PPAQLEFAQFPFL--RGLQKTADFVAISGARAACAEAGQAVHAYPSGSP-FLRWEQ 956
DB 651 -----SPRFILGMKDLVTTMDQTDATMSFREVAARWPEFNVTTF---MPIWMFTDQ 698

QY 957 YLGRRCFLAVCILLVCTFLVCAILLNP-----WTAGLIVLVLAMMTVELFGIMGLF-- 1010
DB 699 YIIIPNTVQNIITALLVMIVIALFTPOPMCSLWVA-----LACASID-FGVIGYMTL 751

QY 1011 -GILSAIPVIVLASVIGVEFTVHALGFLT--QGSRNLRARAAHALEHTFAPYTDGALS 1068
DB 752 WGVNLDALSMITITMSIGFSDYSAHAYGVVSRDTAAGRVEALSGALWPLSQGAMS 811

QY 1069 TLLGLMLAGSHDFIVRYFAALTVTLLGLLHGLVLLPVLISL-----GP 1116
DB 812 TIIAVSLADIAPYMIVT-FEKTVVLISLGLLHGLVFLPVLISIFVRCGCIIPSSPHG 870
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QY 1117 PPEV-----TQMYKESPEILSPAPQGGGLRWGASSSLPQSFAFRTTSMTV 1162
DB 871 PSAQKIEKQIRIAAISSSPLDLRTVAP-----LRASSPISGPHRLEVTDESPTV 919
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RESULT 12

T26746

hypothetical protein Y39A1B.2 - Caenorhabditis elegans

C: Species: Caenorhabditis elegans

C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C: Accession: T26746

R: Wall, M.

submitted to the EMBL Data Library, January 1998

A: Reference number: Z20258

A: Accession: T26746

A: Status: preliminary; translated from GB/EMBL/DBDJB

A: Molecule type: DNA

A: Residues: 1-1003 <WIL>

A: Cross-references: UNIPROT: O9XXR9; EMBL: AL021482; PIDN: CAA16339.1; GSPDB: GN00021; CESP:

A: Experimental source: clone Y39A1B

C: Genetics:

A: Gene: CESP: Y39A1B.2

A: Map position: 3

A: Introns: 89/2; 126/3; 167/2; 194/2; 232/1; 266/3; 295/2; 323/2; 363/1; 519/3; 696/3; 7

Query Match

7.1%; Score 444; DB 2; Length 1003;

Best Local Similarity 21.6%; Pred. No. 1.5e-22;

Matches 214; Conservative 131; Mismatches 333; Indels 312; Gaps 34;

QY 285 GFSHKFMWQEBELLGGHWARDPQGLLRABALQSTFLMSPRLYEHFRGDYQTHDIGMS 344

DB 214 GNTH-----LLGVTLDDDKRIAGAKAMLLPYALR-----HSSDDEW- 251

QY 345 EEOASTVLQAWORRFVQLAQEALPENASQOIHAFSTTLLDILHAFSEVSAARVGVGVL 404

DB 252 -----VAEKWE--VRLA-DFLLQYDSPIRA-SWYIETLA---ASASDRQLQIHL 297

QY 405 MLAYACVTMLRWDC-----QSOGSVGLAGVLLVALAVASGLGLCALGIGITFNAATQV 458

DB 298 LPCFVCVSIFTIACCVCFSWRSPRLAIGGVISAAMAIASAVGILLAGVMTSVAYS- 356

QY 459 LPFLALGIGVDVDFLLAHAFTEALPGTPOERMGECLQRTGTSVVLTSINMAAFMAAL 518

DB 357 MEFIVFSVGVNDVNFILLSAMRSTSTETLEHRMKTETADAASVITVSTLTLISFGVCA 416

QY 519 VPIPALRAFSLQAAIVGCTFVAVMLVFPALISLDLR-----RRCORLDVLCFSSPCSA 574

DB 417 TPFVSQVQFCAYAAVIFTIYIQTFFAAVVMVTNRREINNRHC-----461

QY 575 QVIQILPQELGDTVPVVGIAHLTATVQAFTHCEASSQHVVTILPPQAHVLPSPDPLGSE 634

DB 462 ----IFFHKLKDDTLPEKIA-----477

QY 635 LFSFGSTRDLLQBEETROKAAKSLPCARWNLAFARYQFAPLLQSHAKAIVLVLF 694

DB 478 -----AQRDRSFENNTI-----LAQFFRTTYSDFLLNPLVRIVLVTF 516

QY 695 ALLGLSLYGATLVQDGLALTDVVRGTKEHAFSLAQRLRYFSLYEVALVTQGFYAHQS 754

DB 517 VYLGVASYGCTKVKLGLEPNDDLSPENSYGKRTLMMAKYS-----DYGSS-- 562

QY 755 ALFDLHQRFSSLKAVLPPPPATQAPRTWLHYRNWLQIOAAAFDQW-----ASGRITRHSY 810

DB 563 -----LHVWYNLSEVDVAPRKIWNVLKEVELYEHT 595

QY 811 RNSGEDGALAYKLLIQTGDAQEPLDFSQLTRKLVDREG-LIPELF-YMGLTVMVSSDP 868

DB 596 FTASSDSWLR-----TFLAFVKQAGLLITPENFVILKNVFLSQ-- 634

QY 869 LGLAASQANFYPPPELWHDKYDTT-----GENLRIPPAQLEFAQFPFLRGLQKTADFV 924

DB 635 -----POFAYKYNRQDVLTDEGEH-----LEASRIPVQLR-----HV 665

[illegible]

Db 161 KLAGDNGENIIVEA--TAWLLIYQLKYPN-----EISVSGLWEREFK 203
 QY 361 QLAQALPENASQIIHAFSSTLDDILHAFSEVSAARVVGGLMLLAYACVTML----- 414
 Db 204 NKDEYKQAKYISITYFTISQTLSDENRNERLAPKFGAFVILVCFSLCSIVTIKGS 263
 QY 415 -RWDCAQSGVGLAGVLLVALAVASGLGICALLGTFENAAATTVQLPFLALGVDVDFL 473
 Db 264 GYIDWVVTKPIILSVLGVSNAGIASAGMLTYLEIQYNDITA--VMPFLVAVGTNMF 322
 QY 474 LAHAFTALPGTLPQRMGECIQTGTSVVLTSINNMAAFMAALVPIIPALRAFSIQAAI 533
 Db 323 MVASLRTDRNLKYDORIAECMAADAASLITALTALDALSFGVGTITIPAVQIFCIYTC 382
 QY 534 VVGCTFVAVMLVFPALISLDRRRHQRLDVLCCFSSPCSAQVIQILPQELGDTVPVGI 593
 Db 383 ALLLTAYQITFFCALVY----- 401
 QY 594 AHLTATVQATFHCASSQHWVTILPQAHVLPSPDPLGSELFSPG-----G 640
 Db 402 -----YTRIEGGLHSIMLRPAVY---SSTSPNLVKLFWLGSQKPLPSCGTVS 449
 QY 641 STRDLGQEEETROKAACKSLPCARWNLAFHARYQFAPILLQSHAKAIIVLVFGALLGLS 700
 Db 450 STSSVSTWTSQATSPASKLHCA---ATSFERNWYAPVLMQFWIRAIAGLWYLIYLGIS 506
 QY 701 LYGATLVQDGLALTQV---PRGTEHAFSLAQRYFSLYEVALYTOGDFYAHLS-ORAL 756
 Db 507 YGCTHLKGLPAILVDVDSVATPHYRVLEKHYHYGA-SIQIVVSNPPDLRDPVERIN 565
 QY 757 FD-LHQRFSSSLKAVLPFPATQAPRTWLHYRNWLOGIQAAFPQDQWASGRITRHSYRNGSE 815
 Db 566 MDKMASTFANCAIGDSDVQF-----WLREMQ-----VSEIHKIQDYN--- 605
 QY 816 DGALAYKLLIQTDGAQEPDLSQLTRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQ 875
 Db 606 -----EKFYDHAQAQYIYSD-----MSQ 622
 QY 876 ANFYPPPEWLHD-KYDTTGENLRIPPAQLEFAQFPFLRLGLOQTADFVEAIEGARAC 934
 Db 623 -----PWVVVWVGRRNNSERI-----IKTRFMIQMRDISITTKQTEATNTFREIA 669
 QY 935 AEAGQAGVHAYPGSGP-FLFWEQYGLRRCFLAVCILLVCTFLVALLNPNWTAGLIV 993
 Db 670 SRFEQYNTVY---NPLWLFDOYALVVPNTMQDIIVAVACMLVLSALLIOPQVCSFWVA 726
 QY 994 LVLAMTVELGFMGLGKLSAIPVVLVASVGIGVEFTVHVALGF-LTTQGSNLRAA 1052
 Db 727 VTIGSIDGLVGLFMTLWNVNLDASMITIIMSVPDYSYSAHITVAYVIXESTTSARVC 786
 QY 1053 HALBHTFAPVTDGAISTLLGLLMLAGSHDFIVRYF---FAALTVLTLLGLLHGLVLLPV 1109
 Db 787 DALGDLGWPVAGQAMSTILAVSLSDVPAYMIVTFFTKVFLAISI---GFLHGLVFLPL 842
 QY 1110 LLSI 1113
 Db 843 MLSV 846

RESULT 15

T26521

hypothetical protein Y18D10A.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26521

R:Harris, B.

submitted to the EMBL Data Library, December 1998

A:Reference number: Z20226

A:Accession: T26521

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-936 <WIL>

A:Cross-references: UNIPROT:Q9XW22; EMBL:AL034393; PIDN:CAA22312.1; CESP:Y18D10A.7

A:Experimental source: clone Y18D10A

C:Genetics:

A:Gene: CESP:Y18D10A.7

A:Introns: 11/1; 44/2; 106/1; 166/3; 289/2; 373/1; 396/3; 485/1; 573/3; 615/3; 644/3; 68/

Query Match

Best Local Similarity 6.2%; Score 389.5; DB 2; Length 936;

Matches 186; Conservative 152; Mismatches 339; Indels 247; Gaps 33;

QY 279 LSGCGHGFHK--FMHWQBELLLGGWARDPOCELLR---AEALQSTFILMSPQLYEHPR 333
 Db 149 LLSAGRIPTYKOVCLHFQNDCF-----SNPHAKLLANIYSKHNSMFNIT---YPIIR 199
 QY 334 GYOTHDIGWSE-----EQASTVL-----QAWQ---RRFVQ-LAQEALPEN 370
 Db 200 STYATEPIDISKLVGNVSLDYDGHVENASAWLLIYQLKNEKWLSDRDPEDGLAEKIQSSE 259
 QY 371 ASQQ---THAFSSTLDDILHAFSEVSAARVVGGLMLLAYACVT----- 412
 Db 260 APSELNLYYFHSATFDQELEKENRRLTPKFSITFSVLIIIPAIMTFTTIKFMKFKTENG 319
 QY 413 ---MLRWDCAQSGVGLAGVLLVALAVASGLGICALLGTFENAAATTVQLPFLALGIGV 468
 Db 320 NQYPVIDW--VLSKPLGLIGVLTMCALISTGLMLFNVTVDVDMCT--VMPFLSLTIGI 376
 QY 469 DDVFLAHAFTEALPGTLPQRMGECIQTGTSVVLTSINNMAAFMAALVPIIPALRAFS 528
 Db 377 DDTFLMAAHTEDRNLPEYKRIEKAMRHAASVISITSLDALAFILGSIAPLPAVIYFC 436
 QY 529 LQAAIVVGCCTFVAVMLVFPALISLDRRRHQRLDVLCCFSSPCSAQVIQILPQELGDT 588
 Db 437 YSSAAILFIPLYLTVMFVAVLALQGRREEDLKHSV-----TGMKT 477
 QY 589 VPVGIAHLTAVQATFHCASSQHWVTILPQAHVLPSPDPLGSELFSPGSTRDLGQ 648
 Db 478 IDLSDYETATR-----OLLLKMSRVSVKAD 505
 QY 649 BEETROK-----AACKSLPCARWNLAFHARYQFAPILLQSHAKAIIVLVFGALLGLSYG 703
 Db 506 ENNNNNNEKSIENIKIDNMW-YQRFEDQYAFFISKISILSLFLIYLALYLAFAAFVG 564
 QY 704 ATLVDQD-----LALTVDVPGTKEHAFSLAQRYF---SLYEVALVYQ 744
 Db 565 VKHLKIGDFVTVVLTITIKYVQLINIVQEDSASRVLEVRQFLPBDTKLMDIAVMNS 624
 QY 745 GGFYAHQSORALFDLHQRFSSSLKAVLPFPATQAPRTWLHYRNWLOGIQAAFPDQDQWASGR 804
 Db 625 PNFNSPEER---FNFMEVLSEFESTWCSEGSTQFWFFEMQKYLSD---GFGGDLTK-- 677
 QY 805 ITRHSYRNGSEDGALAYKLLIQTG-----DAQEPDLSQLTRKLVDRGLIPPELFYMG 859
 Db 678 -TMNSERKLSQ---SKTFLMSHEKFGYDVLSDKQFRLSTRLKNVETD---EEMFNCA 728
 QY 860 LTVWVSSDPLGLAASQANF--YPPPEPW-LHKYDVTGTGENLRIPPAQLEFAQFPFLRLG 916
 Db 729 RTM-----RKLQKHANYSIITYSPLWNIADYD----- 757
 QY 917 LQKTADFVEATEGARAACAAGQAGVHAYPGSGPFLFWEQYGLRRCFLAVCILLVCTF 976
 Db 758 -----IMWPQTM---QDIYISIAVMNP--- 776
 QY 977 LVCALLLNPNWTAGLIVLVLAMTVELGFMGLGKLSAIPVVLVASVGIGVEFTVHV 1036
 Db 777 -VALLFIQPLCSVIIIGLNIASTAFVIGTMSFLGVSLDATSMITVAMSVGFSVDFAAHV 835
 QY 1037 ALGFLTTTQGSR-----NLRAAHALEHTPAPVTDGAISTLLGL--LMLAGSHDFIVRY 1087
 Db 836 SYAYMTESGAQIPGKSAYISYRFRCHTGTICWPVTQASVSVLLGVSSLYLVDLS---YVQVT 892
 QY 1088 FFAALTVLTLLGLLHGLVLLPVLL 1111
 Db 893 CFRTVVLVILFGTTHALVFLPLL 916

Search completed: November 22, 2004, 07:58:08
Job time : 32 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 10:37:41 ; Search time 914 Seconds
(without alignments)
7112.209 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPRLRLPSYTPPART.....SPAATSSGNLSRGPGPAG 1203

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QPMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	6248	99.6	4391	9	US-09-909-280A-1 Sequence 1, Appli
3	3955	63.1	4004	9	US-09-990-046-8 Sequence 8, Appli
4	3387	54.0	2082	9	US-09-990-046-9 Sequence 9, Appli
5	3349	53.4	5288	8	US-08-954-701A-18 Sequence 18, Appli
6	3349	53.4	5288	15	US-09-754-032-18 Sequence 18, Appli
7	3349	53.4	5288	15	US-10-421-446-18 Sequence 18, Appli
8	3337	53.2	5187	8	US-08-954-701A-3 Sequence 3, Appli
9	3337	53.2	5187	8	US-08-954-701A-9 Sequence 9, Appli
10	3337	53.2	5187	10	US-09-754-032-3 Sequence 3, Appli
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14	3336	53.2	6568	15	US-10-302-279-1 Sequence 1, Appli
15	3329	53.1	6568	9	US-09-964-824A-266 Sequence 266, App
16	1972.5	31.4	3900	8	US-08-954-771-42 Sequence 42, Appl
17	1972.5	31.4	3900	8	US-08-462-386D-42 Sequence 42, Appl
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20	1956	31.2	4434	8	US-08-954-701A-5 Sequence 5, Appli
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24	640	10.2	4673	16	US-10-172-118-459 Sequence 459, App
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26	640	10.2	4673	17	US-10-776-827-100 Sequence 100, App
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28	627	10.0	3996	16	US-10-621-758A-1 Sequence 1, Appli
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45	602.5	9.6	5029	14	US-10-208-731-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-990-046-1
; Sequence 1, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990.046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 1
; LENGTH: 4030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-990-046-1

Alignment Scores:

Pred. No.:	0	Length:	4030
Score:	6272.00	Matches:	1203
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9	Indels:	0
DB:		Gaps:	0
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QY	21	AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe	40
DB	293	GCAGCACCCAGATCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTGTCTTACTTC	352
QY	41	GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe	60
DB	353	CAGGCGCTTCTCTCTCTGGGATGGGATCCAGAGACATTTGGCAAGTGTCTTT	412
QY	61	LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleLeuThr	80
DB	413	CTGGACTGTTGGCCCTTTGGGCGCCCTGGCATTAGGTCTCCGCATGGCCATTATGAGACA	472
QY	81	AsnLeuGluGlnLeuTrpValGlnValGlySerArgValSerGlnGluLeuHisTyrThr	100
DB	473	AACTTTGGAAACAGCTCTGGGTAGAGTGGGACCGCGGTGAGCAGAGCTGCATTACACC	532
QY	101	LysGluLysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg	120
DB	533	AAGGAGAGCTGGGGAGGAGCTGCATACACTCTCAGATGCTGATACAGACCGCAGCC	592
QY	121	GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu	140
DB	593	CAGGAGGAGAGAACATCTCACCCGGAAGCACCTTGGCCTCCACCTCCAGGAGCCCTC	652
QY	141	ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys	160
DB	653	ACTGCCAGTAAAGTCCAGTATCACTATGGAAGTCTCTGGATTGGAACAAATCTGC	712
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DB	713	TACAGTCAAGATTCCTTATGAAATGNAATGATTTAGTGGATGATTGAGAAGCTG	772
QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly	200
DB	773	TTTCCGTGCTGATCTCACCCCGCTCGACTGCTTCTGGAGGGAGCCAAACTCCAAAGG	832
QY	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220
DB	833	GGCTCCGCTACTCGCCCGCGCCCGCGATATCCAGTGACCAACCTGGATCCAGAGCAG	892
QY	221	LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240
DB	893	CTGCTGGAGAGCTGGGTCCCTTTGGCTCCCTTGAGGGCTTCGGGAGCTGTAGACAAG	952
QY	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisPheProAspLeuHisCys	260
DB	953	GCACAGTGGCCAGGCTACGTGGGCGCGCCCTGTCTGCACCCCTGATGACCTCCACTGC	1012
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280
DB	1013	CCACCTAGTGGCCCCAACCATACAGCAGGAGGCTCCCAATGTGGCTCAGAGCTGAGT	1072
QY	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuLeuGly	300
DB	1073	GGGGGCTGCATGGCTTCTCCCAATTCATGCACTGGCAGGAGGAATTTGCTGTGGGA	1132
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320
DB	1133	GGCATGGCCAGAGACCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTCGAGACACCTTC	1192

QY	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340
DB	1193	TTGCTGATGATCCCGCCAGCTGTACAGCATTTCCGGGGTGACTATCAGACACATGAC	1252
QY	341	IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal	360
DB	1253	ATTGCTGGAGTGGAGGAGCAGCCAGACAGTGTCTACAAGCTGGCAGCGGCTTTGTG	1312
QY	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380
DB	1313	CAGCTGGCCCGAGGAGGCTCCCTGAGAACCTTCCAGCAGATCCATGCGCTTCTCCCTCC	1372
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400
DB	1373	ACCACCTGGATGACATCTGCATGGCTTCTGAAGTCAGTGTCCCGTGTGTGGGA	1432
QY	401	GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln	420
DB	1433	GGCTATCTGCTCATGCTGGCCTATGCTGTGTGACCATGCTGCGGTGGGACTGCGCCAG	1492
QY	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly	440
DB	1493	TCCGAGGCTTCGTGGGCTTTCGCGGGGTACTGTGTGGGCTTCGCGGTGCGCTCAGGC	1552
QY	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrGlnValLeuPro	460
DB	1553	CTTGGGCTCTGTGCGCTGCTGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCT	1612
QY	461	PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu	480
DB	1613	TTCTTGGCTCTGGGAATCGGTGATGACGTATTCTCTGCTGGCGATGCTCTCACAGAG	1672
QY	481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr	500
DB	1673	GGCTTGGCTGGCACCCTCTCCAGAGCGCATGGGCGAGTGTCTCAGCGCAGCGGCACC	1732
QY	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro	520
DB	1733	AGTGTGCTACTCACATCCATCAACATGGCGGCTTCTCTCATGGCTGCGCTGCC	1792
QY	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540
DB	1793	ATCCCTCGCTCGAGCGCTTCTCCCTACAGCGCGCATAGTGTGTGGCTGCACCTTTGA	1852
QY	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560
DB	1853	CGCTGTGCTGTGTCTTCCAGCCCATCTCAGCCTGGACCTACGGCGGCGCCACTGCCAG	1912
QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
DB	1913	CGCCTTGATGCTCTGTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAAGTCTG	1972
QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
DB	1973	CCCCAGGAGCTGGGAGCAGGACAGTACCAGTGGGCATTGCCACCTCTCAGCCAGTT	2032
QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
DB	2033	CAAGCCTTTACCACCTGTGAGCAGCAGCAGCATGTGGTCACCATCTCTGCTCCCAA	2092
QY	621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
DB	2093	GCCCACTGGTGGCCCACTTCTGACCCACTGGGCTCTGAGCTCTTACGCTGAGGG	2152
QY	641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer	660
DB	2153	TCCACACGGGACCTTCTAGCGCAGGAGGAGAGACAAGGCAAGGACGCTGCAAGTCC	2212
QY	661	LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
DB	2213	CTGCCCTGTGCCGCTGGGAATCTTGGCCATTTGCCCGCTATCAGTTTCCCGCTGCTG	2272
QY	681	LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700


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Db      2273  CTCCAGTCACATGCCAAGGCCATCGTGTGCTCTTTGGTGTCTCTTCTTGCGGCTGAGC 2332
QY      701    LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db      2333  CTCTACGGAGCCACCTTGGTGCAGAGCGGCTGGCCCTGACGATGTGTGTGCTCGGGC 2392
QY      721    ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db      2393  ACCAAGGAGATGCCCTTCTGAGGCGCCAGCTCAGGTACTTCTCCCTGTACAGAGGTGGCC 2452
QY      741    LeuValThrGlnGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db      2453  CTGGTGACCCAGGGTGGCTTGACTAGCCCAATTCCCAACGGCCCTCTTTGATCTGCAC 2512
QY      761    GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr 780
Db      2513  CAGCGCTTCAGTTCCCTCAAGGGGGTGTGTCGCCCAACCGGCCACCCAGGCACCCGCACC 2572
QY      781    TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyLeuGlnAlaAlaPheAspGlnAspTrp 800
Db      2573  TGGCTGCATTAATACCGCACTGGCTACAGGGAATCCAGGCTGCCCTTGACAGGACTGG 2632
QY      801    AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db      2633  GCTTCTGGGCGCATCACCGGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692
QY      821    TyrLysLeuLeuLeuLeuGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db      2693  TACAGCTGCTCATCCAGACTGAGACGCCCGGAGCCCTCTGGATTTCAGCCAGCTGACC 2752
QY      841    ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db      2753  ACAAGGAACCTGGTGACAGAGGAGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812
QY      861    ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db      2813  ACCGTGTGGTGAGCAGTACCCCTCGGTCTGGCAGCCTCAGAGCCAACTTCTACCCC 2872
QY      881    ProProGluTrpLeuHisAspLysTyrAspThrThrGlyLeuAsnLeuArgIlePro 900
Db      2873  CCACCTCTCGAATGGCTGCACACAAATACGACACACCGGGGAGAACCTTCGCATCCGG 2932
QY      901    ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db      2933  CCAGCTACGCCCTTGAGATTGCCAGATTCCCTTCTCTGCTCGGTGGCCCTCAGAGACT 2992
QY      921    AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db      2993  GCAGACTTTGTGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGCGCCGCGAGCT 3052
QY      941    GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db      3053  GGGGTGACGGCTACCCCGAGGGCTCCGCCCTTCCTCTTCTGGGAACAGTATCTGGGCGTG 3112
QY      961    ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db      3113  CGGGCTGCTCTTCTGCTGGCGCTGTCATCTCTGCTGTGTGCACTTCTCTGCTGTGCT 3172
QY      981    LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db      3173  CTGCTGCTCTCAACCCCTCGAGCGGCTGGCCTCATAGTGTGCTGCTGGCGATGATGACA 3232
QY      1001  ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db      3233  GTGGAACCTCTTTGGTATCATGGGTTTCTCGGCGCATCAAGCTGAGTGCATCCCGGTGGT 3292
QY      1021  IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db      3293  ATCCTTGGGGCTCTGTAGGCATTTGGCGTTGAGTTTCAGTCCACGTCAGTGGCTTCGGGCTTC 3352
QY      1041  LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060

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Db      3353  CTGACACACCCAGGGCAGCCGGAAACCTGCGGGCCGCCCATGCCCTTGACGACACATTTGCC 3412
QY      1061  ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db      3413  CCGCTGACCGATGGGCCATCTCCACATGCTGGGTCTGCTCATGTGCTTGTGGTCCAC 3472
QY      1081  PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db      3473  TTTGACTTCAATTAAAGTACTTCTTTGGGCGCTGACAGTGCTCAGCTCCTTGGGCGTC 3532
QY      1101  LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
Db      3533  CTCCATGGACTCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3592
QY      1121  IleGlnMetTyrLysGluSerProGluIleLeuSerProAlaProGlnGlyGlyGly 1140
Db      3593  ATACAGATGTACAAAGAAAGCCAGAGATCTTGAGTCCAGCTCCAGAGAGTACCTCCATG 3652
QY      1141  LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db      3653  CTTAGGTGGGGGCGCATCTCTCTCCCTGCGCCAGAGCTTTGCCAGAGTACCTACCTCATG 3712
QY      1161  ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db      3713  ACGTGGCCATCCACCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3772
QY      1181  ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db      3773  CCCCCCTTGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3832
QY      1201  AlaThrGly 1203
Db      3833  GCCACTGGG 3841

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RESULT 2

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US-09-909-280A-1
; Sequence 1, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
; APPLICANT: Bumcroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297) .. (3905)
US-09-909-280A-1

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Alignment Scores:
Pred. No.: 0 Length: 4391
Score: 6248.00 Matches: 1200
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 3
Query Match: 99.62% Indels: 0
DB: 9 Gaps: 0

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US-09-990-046-2 (1-1203) x US-09-909-280A-1 (1-4391)

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QY      1    MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
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QY	21	AlaAlaProGlnIleLeuAlaGlySerLeuIlysAlaProLeuTrpLeuArgAlaTyrPhe	40
DB	357	GCAGACCCAGATCCTAGCTGGAGCCTGAAGGCTCCACTCTGGCTTCGTCTTACTTC	416
QY	41	GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyIysValLeuPhe	60
DB	417	CAGGCGCTGCTCTCTCTGGATGCGGGATCCAGAGACATTGGCAAAATGCTCTTT	476
QY	61	LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleLeuThr	80
DB	477	CTGGACACTGTTGGGCGCTTGGGCGCTTGGATTAGGCTCCGCAATGATTTAGACAC	536
QY	81	AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr	100
DB	537	AACTTGGAAACAGCTCTGGGTAGAGTGGGAGCGCGGTGAGCGAGGTGATTAACACC	596
QY	101	IysGluIysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg	120
DB	597	AAGGAGAGCTGGGAGAGGCTGCATACACTCTCAGATGCTGATACAGACCGACGC	656
QY	121	GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisIleuGlnAlaLeu	140
DB	657	CAGGAGGAGAGACATCTCACCCGAGACACTTGGCTCCACCTCCAGGCGAGCCCTC	716
QY	141	ThrAlaSerIysValGlnValSerLeuTyrGlyIysSerTrpAspLeuAsnIysIleCys	160
DB	717	ACTGCCAGTAAAGTCCAAAGTATCACTCTATGGAAAGTCTGGGATTTGAACAAATCTGC	776
QY	161	TyrIysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluIysLeu	180
DB	777	TACAAGTCAGGAGTCCCCCTTATTTGAANAATGNAATGATTGAGCGGATGATTGAGAAGCTG	836
QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaIysLeuGlnGly	200
DB	837	TTTCCGTGGTGATCTCACCCCTCGACTGCTTCTGGGAGGAGCCAAACTCCAAAGG	896
QY	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220
DB	897	GGCTCGGCCTACCTGCCCGCGCGCGGATATCCAGTGACCAACCTGGATCCAGAGCAG	956
QY	221	LeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240
DB	957	CTGCTGGAGAGCTGGGTCCCTTTGGCTTCCCTTGAGGGCTTCCGGAGCTGTAGACAAG	1016
QY	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys	260
DB	1017	GCACAGTGGCCAGGCTAGGTGGGGGCGGCTGTCTGCACCTGATGACCTCCACTGC	1076
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280
DB	1077	CCACCTAGTGCCCGCCCAACATCAAGAGAGGCTCCCAATGTGGCTCAGAGCTGAGT	1136
QY	281	GlyGlyCysHisGlyPheSerHisIysPheMetHisTrpGlnGluLeuLeuLeuGly	300
DB	1137	GGGGGTGCATGGCTTCTCCCAAAATTCATGCATGGCAGAGGAAATGCTGCTGGGA	1196
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320
DB	1197	GGCATGGCCAGAGACCCCAAGGAGAGCTGCTGAGGGCAGAGGCGCTGCAGAGCACCTTC	1256
QY	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340
DB	1257	TTGCTGATAGTCCCGCCAGCTGTACAGCATTTCCGGGGTGACTATACAGACATGAC	1316
QY	341	IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal	360
DB	1317	ATTGGCTGGAGTGAGGAGCAGGCAGACAGTGTCTACAGCCTGGCAGCGCGCTTTGTG	1376
QY	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380
DB	1377	CAGCTGGCCAGGAGGCGCTGCCTGAGACGCTTCCAGCAGATCCATGCTCTCTCTCC	1436
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400
DB	1437	ACCACCCCTGGATGACATCTGTCATCGCTTCTCTGAAGTCAGTGTGCCGTGTGTGGGA	1496
QY	401	GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln	420
DB	1497	GGCTATCTGCTCATGCTGGCTATGCTGTGTGACCATGCTGCGGTGGAGACTGCGCCAG	1556
QY	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly	440
DB	1557	TCCCAAGGTTCCGTGGGCTTCCCGGGGTACTGCTGGTGGCCCTGGCGTGCCTCAGGC	1616
QY	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro	460
DB	1617	CTTGGGCTCTGTGGCTGCTCGGCATCACCTTCAATGTGCCACTACCCAGGTGCTGCC	1676
QY	461	PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu	480
DB	1677	TTCTTTGGCTCTGGGAATCGGCTGGATGACGTATTCTCTGCTGGCGCATGCCCTTCAGAG	1736
QY	481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyThr	500
DB	1737	GCTCTGCCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCGCACCC	1796
QY	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro	520
DB	1797	AGTGTGCTACTCACATCCATCAACAACATGGCCGCTTCTCATGGCTGCCCTCGTTCCC	1856
QY	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540
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QY	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560
DB	1917	GGCGTAGTCTGTCTTCCAGCCATCTCAGCTTGGACTTACGGCGGCGCCACTGCCAG	1976
QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
DB	1977	CGCCTTGATGCTCTGTCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTAGATCCTG	2036
QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
DB	2037	CCCCAGAGCTGGGGAGCGGACAGTACCAGTGGGCAATTGCCACCTCTCATGCGACAGTT	2096
QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
DB	2097	CAGCCCTTACCACCTGTGAGCGCAGCAGCCAGCATGTGTCACCATCTGCTGCCCTCCCAA	2156
QY	621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
DB	2157	GCCACCTGGTGCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCCAGCCCTGGAGGG	2216
QY	641	SerThrArgAspLeuLeuGlnGluGluThrArgGlnIlysAlaCysIysSer	660
DB	2217	TCCACACGGGACCTTCTAGGCCAGGAGGACCAAGGAGGAGCGCTTCCAGTCC	2276
QY	661	LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
DB	2277	CTGCCCTGTGCCCGCTGGAAATCTTGCCCATTTCCCGCGTATCAGTTGCCCCGTGCTG	2336
QY	681	LeuGlnSerHisAlaIysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700
DB	2337	CTCCAGTCAATGCCAAGGCCATCGTGTGCTCTTTGGTGTCTCTTCTGGGCTGAGC	2396
QY	701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaIleuThrAspValValProArgGly	720
DB	2397	CTCTACGGAGCCACTTGGTGCAGAGCGCTCGCCCTTGACGATGTGCTGCTCGSGGC	2456
QY	721	ThrIysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740
DB	2457	ACCAGGAGCATGCTCTCTGAGCGCCAGCTCAGGTACTTCTCTCTGTGTAGAGGTGCC	2516
QY	741	LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis	760

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 Db 3897 GCCACTGGG 3905
 RESULT 3
 US-09-990-046-8
 ; Sequence 8, Application US/09990046
 ; Patent No. US20020156245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: de Sauvage, Frederic
 ; APPLICANT: Carpenter, David A.
 ; TITLE OF INVENTION: Patched-2
 ; FILE REFERENCE: P1405R1
 ; CURRENT APPLICATION NUMBER: US/09/990,046
 ; PRIOR FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
 ; NUMBER OF SEQ ID NOS: 32
 ; SEQ ID NO 8
 ; LENGTH: 4004
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-990-046-8
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 Score: 3955.00 Matches: 847
 Percent Similarity: 65.81% Conservative: 2
 Best Local Similarity: 65.66% Mismatches: 10
 Query Match: 63.06% Indels: 434
 DB: 9 Gaps: 10
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 11 CGGGAGAAGCTGGGGAGAGGCTGCATACCTCTCAGATGCTCATACAGACCGCACGC 70
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 Db :
 71 CAGGAGGAGAGAACATCTCACCCGAAGACATTTGGCTCCACTCCAGCGAGCCCTC 130
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTirPaspLeuAsnIlysIleCys 160
 Db ACTGCCAGTAAGTCCAAGTATCACTCTATGGGAAGTCTCTGGATTTGAAACAATACTGCG 190
 QY 161 TyrLysSerGlyValProLeuIleGlnAsnGlyMetIleGluTrpMetIleGluLysLeu 180
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 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
 Db TTTCGTGCGTGATCTCACCCCCCTCGACTGCTTCTGGGAGGAGGCCAACTCCAAGGG 310
 QY 201 GlySerAlaTyrLeuProGlyArgProAspileGlnTrpThrAsnLeuAspProGluGln 220

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Db	330	-----	330	Db	1255	TCTGAGGAGCTCAGCTTACTTGGTTAAGAGCCTCTTGGTTCAAAGTGACCTTGGGCTGCTA	1314	
Qy	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys	260	Qy	485	485	-----	485
Db	330	-----	330	Db	1315	ATGAACCTCGTGCTCTTGTGCCCATGTGTAAACAGGGGAAATAATAGTGTGTCTCT	1374	
Qy	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280	Qy	485	485	-----	485
Db	331	-----	331	Db	1375	AAGGTTATTGTTGGATCAGTGAAGTAACCTCAAGTTGAATGCTTAGAACAGCCCATCAT	1434	
Qy	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuGly	300	Qy	485	485	-----	485
Db	355	GGGGCTGTCATGGCTTCTCCACAAATTCATGCATGGCAGGAGAAATTGCTGTGGGA	414	Db	1435	ACGTACATGTTACCCATAAATGCTAGCCACTGTGTATGACTGCCCCACCTCTGCACCC	1494	
Qy	301	GlyMetAlaArgAspProGlnGlyLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320	Qy	485	485	-----	485
Db	415	GGCATGGCCAGAGACCCCAAGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC	474	Db	1495	CAAAGTTCTGTAGCCCTCCCTTCACTCCACTTTTGACACGGCCCTCCCTTGTGACCTGAGG	1554	
Qy	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340	Qy	486	-----	486	486
Db	475	TTGCTGATGATGATCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC	534	Db	1555	GCAGGTCCCCACTCTGTCTCTGG- CAGGAGCGCATGGGGAGTGTCTGCAGCGCAGCGGCA	1613	
Qy	341	IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal	360	Qy	500	hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP	520	
Db	535	ATTGGCTGGAGTGGAGGAGCAGCAGCAGTGTCTACAAGCCTGGCAGCGGGCTTTGTG	594	Db	1614	CCAGTGTGTGATCATCATCCATCAACATGGCCGCTTCTCATGGTGCCTCGTCTTC	1673	
Qy	360	-----	360	Qy	520	roileProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV	540	
Db	595	CAGTCCGTATGGACAAGACAGAGGGGGTGCCTGAGGGCATTCCTCTCTGCCCTC	654	Db	1674	CCATCCCTCGCTGGAGCCTTCTCC	1699	
Qy	361	-----	361	Qy	540	alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgHisCys	559	
Db	655	CCTATCCACCTGTTTCTCCAGCTGGCCAGGAGGCCCTGCTGAGAACGCTTCCAGCA	714	Db	1700	-----	1700	
Qy	374	nleHisAlaPheSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe	394	Qy	560	GlnArgLeuAspValLeuCysCysPheSer	569	
Db	715	GATCCATGCTTCTCTCCACACACCTGGATGACATCTGCTGCGTCTCTGAAATCAG	774	Db	1731	CAGCGCTTGAATGTCTCTGTCTGTCTTC- CAGGTACTGCTGGGCCCGCCCTTCTCT	1789	
Qy	394	rAlaAlaArgValValGlyTyrLeuLeuMet	405	Qy	569	-----	569	
Db	775	TGTCCTCGGTGTGGAGGCTATCTGCTCATGGTGGGTCTTGACCTGGCACCTTGCC	834	Db	1790	CCCGTGACCCAGCCAGCCTGTCCCTCACAGCATTTCAAGGCACAGACCTGTCTATCCA	1849	
Qy	405	-----	405	Qy	570	-----	570	
Db	835	CCACCCACCTCCAAACAGTGCCACCCCTGGGGAGGCCCTGAGACTGCCCTTTCCTCC	894	Db	1850	CTCTCTACCTCTTCCAGTCCCTGCTCTGTCTCAGGTGATTAGATCTGCCCGCCAGGAGCTG	1909	
Qy	406	-----	406	Qy	585	GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr	604	
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Qy	424	rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyCys	444	Qy	605	HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal	624	
Db	955	CGTGGGCTTGGCGGGTACTGCTGTGGCCCTGGGGGTGGCCTTCAGGCTTGGGCTCTG	1014	Db	1970	CAGTGTGAAGCCAGCAGCAGCATGTGGTCAACATCTCTGCTCCCAAGCCACCTGGTG	2029	
Qy	444	sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr	456	Qy	625	ProProSerSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644	
Db	1015	TGCCCTGTGCGCATACCTTCAATGTGCCACTACCCAGGTACGCCAGGAGTGCAGGGC	1074	Db	2030	CCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTTCAGCCCTGGAGGTTCCACAGGGAC	2089	
Qy	457	-----	457	Qy	645	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664	
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Qy	457	-----	457	Qy	665	ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis	684	
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Qy	477	laPheThrGluAlaLeuProGlyThr	485	Qy	685	AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla	704	
Db	477	laPheThrGluAlaLeuProGlyThr	485	Db	2210	GCCAAGGCCATCGTGTGCTCTTCTGCTGCTCTTCTGCGCTGAGCTCTACGGAGCC	2269	

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 QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
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 RESULT 4
 US-09-990-046-9
 ; Sequence 9, Application US/09990046
 ; Patent No. US20020156245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: de Sauvage, Frederic
 ; APPLICANT: Carpenter, David A.
 ; TITLE OF INVENTION: Patched-2
 ; FILE REFERENCE: P1405R1
 ; CURRENT APPLICATION NUMBER: US/09/990,046
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
 ; NUMBER OF SEQ ID NOS: 32
 ; SEQ ID NO 9
 ; LENGTH: 2082
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-990-046-9
 Alignment Scores:
 Pred. No.: 3,35e-308 Length: 2082
 Score: 3387.00 Matches: 656
 Percent Similarity: 96.33% Conservative: 1
 Best Local Similarity: 96.13% Mismatches: 3
 Query Match: 54.00% Indels: 23
 DB: 9 Gaps: 2

US-09-990-046-2 (1-1203) x US-09-990-046-9 (1-2082)

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 Db 68 GCAGCACCCAGATCTAGCTGGAGCCTCAAGGCTCCACTCTGGCTTCTGCTTACTTC 127
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 Db 128 CAGGCGCTGCTCTTCTCTCTGGGATGGGGATCCAGAGACATTGTGGCAAAAGTCTCTT 187
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 QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
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 QY 101 LysGlnLysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 Db 308 AAGGAGAAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCAGC 367

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121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
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Db
1981 CTGCAG 1986
RESULT 5
US-08-954-701A-18
; Sequence 18, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709

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[illegible]


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QY 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
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QY 944 AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys 963
Db 3405 AGTTACCCACACGGCTACCCCTTCTCTTCGGAGCAGTACATCGGCCCTCCGCCACTGG 3464
QY 964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db 3465 CTGCTGCTTTCATCAGCGCTGTGGCTCGACATTCCTCTGTGTGCGCTGCTTCCTTT 3524
QY 984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db 3525 CTGAACCCCTGACGCCCGGGATCATGTGATGCTCTCGCGCTGATGACGGTTCGAGCTG 3584
QY 1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
Db 3585 TTCGGCATGATGGCCTCATCGAATCAAGCTCAGTGCCTGCGCGTGCCTGCTCATCTGATC 3644
QY 1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db 3645 GCTTCTGTTGGCATAGGAGTGGAGTTCACCGTTTCAGTTGCTTGTGCGCTTTCGACGGCC 3704
QY 1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db 3705 ATCGCGCAGCAAGAACCGCAGGCTGTGCTTGCCTGGAGCAGCATGTTGCACCGCTCTG 3764
QY 1064 AspGlyAlaIleSerThrLeuLeuGlyLeuMetLeuAlaGlySerHisPheAspPhe 1083
Db 3765 GATGGCGCGTGTCCACTCTGTGGAGTGTCTGATGCTGGCGGATCTGAGTTTCGACTTC 3824
QY 1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
Db 3825 ATTGTCAAGTATTTCTTGTGCTGGCGATCCTCACCATCTCGCGCTTCTCAATGGG 3884
QY 1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal-IleGlnMe 1123
Db 3885 CTGGTTTGTCTCCCGTCTTTTGTCTTCTTCTTGGACCATATCTCGAGGTGTCTCCAGCC 3944
QY 1123 tTyrLys-----GluSerProGluIleLeuSerProAlaLeuProGlnGlyG 1139
Db 3945 AACGGCTTGAACCGCCTGCCACACCTCCCTCCAGCCACCCCGGCG----- 3993
QY 1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db 3994 -----TGTCGCGCTTCGCCATGCCCGCG-----GCCAC 4022
QY 1159 rMetThrValAlaIleHisPro----- 1167
Db 4023 ACGCACAGCGGCTGTATTCCTCCGACTCGGAGTATAGTTCCACAGCAGCAGTGTCAAGC 4082
QY 1168 -----ProLeuProGlyAlaTyrIleHisProAlaProAspG 1180
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436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaIaThr	455	773	oAlaThrGlnAlaProArgThrTrpLeuHisTyrTrpArgAsnTrpLeuGlnGlyIleG1	793
1492	TCAGTGGCTGGAGATTGGCGCTCTCTCTGATTGGCATTTCTTTTAATGCTGGACA	1551	2562	GAACAAGCAACTTCCCAAAATGTGGCTGCACTACTTTAGACAGCTGGCTTCAAGACTTCA	2621
456	ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAla	475	793	nAlaAlaPheAspGlnAspTrpAlaSerGlyArgGlyIleThrArgHisSerTyrArgAsnG1	813
1552	ACTCAGGTTTGGCGTTCTTCTGCTTGGTGTGGTGTGGATGATGCTTCTCTCTGGCC	1611	2622	GGATGCATTTGACAGTGACTGGGAAACATGGGAGGATCATGCCAACAACTATATAAATGG	2681
476	HisAlaPheThrGlnAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGlu	493	813	ySerGlnAspGlyAlaLeuAlaIleTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr	833
1612	CATGCATTCAAGCAAGACAGACAGATAAGAGGATTCATTTGAGACAGGACTGGGAG	1671	2682	ATCAGATGACGGGTCTCTCGCTTACAACTCTCTGGTGACAGCTGGCAGCAGACAAGCC	2741
494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe	513	833	oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr	853
1672	TGCGCTCAAGCGCACCGGACGACGCGGCGCTCACCTCCATCAGCAATGTCACCGCTTC	1731	2742	CATCGACATTAGTCAGTTGACTAAACAGCGTCTGGTAGACGAGATGGCATCAATTAATCC	2801
514	LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle	533	853	oGlnLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl	873
1732	TTCATGGCGCANTGATCCCTATCCCTGCGCTCGAGCGTTCTCCCTCCAGGCTGTGTG	1791	2802	GAGCGCTTCTACATCTACCTGACCGCTTGGGTTCAGCAACGACCTGTAGCTTACGCTGC	2861
534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp	553	873	aSerGlnAlaAsnPheTyrProProProGluTrpLeuHisAspLysTyrAspThrTh	893
1792	GTGGTGTATTCAATTTTGTATGTTCTGCTCATTTTCTGCAATTTCTCAGCATGGAT	1851	2862	CTCCAGCGCAACATCCGCGCTCACCGCGGAGTGGGTCCATGACAAAGCCGATACAT	2921
554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer	573	893	RGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh	912
1852	TTATACAGCGTGGAGACAGAGATTGGATATTTTCTGCTGTTTTCACAGCCCTGTGC	1911	2922	GCCAGAGACCGCTGAGAATCCAGCAGCAGAGCCCATCGAGTACGCTCAGTTCCTCTT	2981
574	AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyI1	593	912	eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl	932
1912	AGCAGGTTGATTCAAGTTGAGCCACAGCGCTACACAGAGCCTCACAGTACACCCGGTAC	1971	2982	CTACCTCAACCGCTACGAGACACCTCAGACTTCTGGAGGCGCATAGAAAAAGTGAGAGT	3041
593	eAla-----HisLeuThrAlaThrValGln-----	601	932	aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe	952
1972	AGCCCCCACCCTATACACAGCCACAGCTTGCCCCACAGAAACCCCATATCACTATGCAG	2031	3042	CATCTGTAAACAATATACAGCGCTGGAGCTGTCCAGCTACCCCAATGGCTACCCCTCTCT	3101
602	----AlaPheThrHisCysGlnAlaSerSerGlnHisValValThrIleLeuProG1	620	952	uPheTrpGlnGlnTyrLeuGlyLeuArgCysPheLeuLeuAlaValCysIleLeuLe	972
2032	TCCACCGTTTTCAGCTCCGACAGAGATTGACCCCTCACACGACGCTGTACTACACACCGCC	2091	3102	GTTCTGGGAGCAATATACATCAGCTTCGCCACTGGCTGTCTGTATCCATCAGCGTGTGTCT	3161
620	nAlaHis-----LeuValProProSerAspProLeuGlySe	633	972	uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuI1	992
2092	GAGCCACGCTCTGATCTCTGTACAGCTGTGTACCTGACCCAG-GACAACTCAGCTG	2150	3162	GGCTCAGCGTTTCTAGTGTGCGAGCTTCTCTCTGAAACCCCTTGACGCGCGGATCAT	3221
633	rgluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThrAr	653	992	eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyI1	1012
2151	TCAGAGTCCGAGAGCACCGCTCTACAGGACCTGCTCTCCAGTTCTCAGACTCC--	2208	3222	TGTCATGGTCTGGCTCTGATGACCGCTGAGCTCTTTGSCATGATGGGCTCATTTGGAT	3281
653	gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr	673	1012	elysLeuSerAlaIleProValValLeuValAlaSerValGlyIleGlyValGluPh	1032
2209	----AGCTCCACTCGCCTCGAGCCCCCTGCACCAAGTGGACACTCTCTGTTGTGAGA	2264	3282	CAAGCTGAGTGTGTGCTGTGCTCATCTCTGATTTGATCTGTGGCATCGGAGTGAGTT	3341
673	gTyrGlnPheAlaProLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh	693	1032	eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl	1052
2265	GAAGCACTATGCTCTTCTCTCTGAAACCCCAAGGTTGTGGTATTCCTCTTTT	2324	3342	CACCGTCCACGCTTGGCTTTCTGACAGCCATTTGGGACACAAAGAACACAGGGCTAT	3401
693	eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrIleuValGlnAspGlyLeuAlaLe	713	1052	aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuG1	1072
2325	CTGGGCTGTGGGGTGACCTTTATGGGACCCACCGAGTGAGAGACGGCTGGACCT	2384	3402	GCTCGCTCTGGAACATGTTTCTCCGTTCTGGAGCGGTGCTGTCTCCACTCTGTGGG	3461
713	uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy	733	1072	yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe	1092
2385	CACGGACATTGTTCCCGGGGAAACAGAGAAATATGACTTCATAGCTGCCAGTTTCAAGTA	2444	3462	TGTACTGATGCTTGCAGGGTCCGAATTTGATTTTATTGTCAGATACTTCTTTGCCGCTCT	3521
733	rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerG1	753	1092	uThrValLeuThrLeuLeuGlyLeuHisGlyLeuValLeuLeuProValLeuLeuSe	1112
2445	CTTCTCTTCTACAACTGTTATAGTCCCCAGGAACCA-----GACTACCCGATATCCA	2501	3522	GGCCATTCTCACCGTCTTGGGGTCTCTCAATGAGACTGGTCTGCTGCTGCTCTTATTC	3581
753	nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr	773	1112	rIleLeuGlyProProGlnValIle-----GlnMetTyrLysG1	1126
2502	GCACCTACTTTACGACCTTCATAGAGTTTCAGCAATGTGAAGTATGTATGCTGGAGGA	2561	3582	CTTCTTTGGACCGTGTCTGAGGTGTCTCCAGCAATGGCTAAACCGACTGCCACTCC	3641
			1126	userProGluIleLeuSerProPro-----AlaProGlnGlyGlyGlyLe	1141

Db 3642 TTCGCTAG-----CGCCTCAAGTGTGTCGGTTTCGGCGCTCTGGTCACAC 3695
 Qy 1141 uArgTIPGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
 Db 3696 GAACAATGGGTCTGATTCCTCCGACTCGGAGTACAGCTCTCAGACCACGGTGTCTGGCAT 3755
 Qy 1159 ----- 1159
 Db 3756 CAGTGAGGAGCTCAGCAATACGAGCACACAGCGGTGCCGAGGCCCTGCCACCAAGT 3815
 Qy 1160 ---MetThrValAlaIleHisProProLeuProGlyAlaTyrIleHisPro---Al 1177
 Db 3816 GATTGTGAAGCCACAGAAACCCCTGTCTTGTCCCGGTCCACTGTGTCCATCGGACTC 3875
 Qy 1177 aProAspGluProProTrpSerProAlaAla-----ThrSerSerGlyAsnLeuSe 1194
 Db 3876 CAGCATCAGCTCCCTTGACCCCTCGGCAACAGCCCCACTGGACTCTGGCTCTGTGTC 3935
 Qy 1194 rSerArgGlyProGly 1199
 Db 3936 C-----CCTGGA 3942

RESULT 9

US-08-954-701A-9
 ; Sequence 9, Application US/08954701A
 ; Publication No. US20030032085A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V
 ; APPLICANT: JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley, Hoag & Eliot
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII(text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/954,701A
 ; FILING DATE: 20-OCT-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36709
 ; REFERENCE/DOCKET NUMBER: SUV-003.08
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5187 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-954-701A-9

Alignment Scores:
 Pred. No.: 6.28e-303 Length: 5187
 Score: 3337.00 Matches: 677
 Percent Similarity: 69.59% Conservative: 204
 Best Local Similarity: 53.48% Mismatches: 306
 Query Match: 53.20% Indels: 80
 DB: 8 Gaps: 20

US-09-990-046-2 (1-1203) x US-08-954-701A-9 (1-5187)
 Qy 3 ArgSerProLeuArgGluLeu-----ProProSerTyrThrProProAlaArgThr 20
 Db 178 CGCGCCGCGCGGACCGGACTATCTGCACCGGCCAGCTACTGC-----GACGCCGCCCTTC 234
 Qy 21 AlaAlaProGlnIleLeuAlaGlySerLeu-----LysAlaProLeuTyrPheArg 37
 Db 235 GCTCTGGAGCAGATTTTCAAGGGGAGGCTACTGGCCGGAAGCGCGCTCTGGCTGAGA 294
 Qy 38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
 Db 295 GCGAAGTTTCAGAGACTCTTATTAACTGGGTGTACATTCAAAGAGACTGCGGGAAG 354
 Qy 58 ValLeuPheLeuGlyLeuLeuAlaPheGlyValAlaLeuAlaLeuGlyLeuArgMetAlaIle 77
 Db 355 TTTTGGTGTGGGTCTCCTCATATTGGGGCCCTCGCTGTGGATTAAAGGAGCTTAAT 414
 Qy 78 IleGluThrAsnLeuGluGlnLeuTyrValGluValGlySerArgValSerGlnGluLeu 97
 Db 415 CTCGAGACCAACGTGGAGGAGCTGTGGTGAAGTTGGTGGACGAGTGAGTCGAGATT 474
 Qy 98 HisTyrThrLysGluLysLeuGlyGluAlaTyrThrSerGlnMetLeuIleGln 117
 Db 475 AATTATACCCGTGAGAAGATAGGAGAGGCTATGTTTAATCTCTCAACTCATGATACAG 534
 Qy 118 ThrAlaArgGlnGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGln 137
 Db 535 ACTCCAAAGAGAGCGCTAATGTCTGACACAGAGGCTCTCTGCAACACCTGGAC 594
 Qy 138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTyrAspLeuAsn 157
 Db 595 TCAGCACTCCAGGCCAGTCGTGTCACGCTCATCTATATAACAGGCAATGGAAGTTGGA 654
 Qy 158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle 177
 Db 655 CATTTGTCTACAAATCAGGGGAACCTTATCAGGAGACAGGTATCATGATCAGATAATA 714
 Qy 178 GluLysLeuPheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197
 Db 715 GAATACCTTTACCTTGTCTAATCATTCATCCTTTGGACTGTCTCTGGGAAGGGGAAAG 774
 Qy 198 LeuGlnGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217
 Db 775 CTACAGTCGGGACAGCATACCTCTAGTAAGCTCTCTTACGGTGGCAACCTTTGAC 834
 Qy 218 ProGluGlnLeuLeuGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236
 Db 835 CCTTGGAAATTCCTAGAAGAGTTAAAGAAATAAACTACCAAGTGGACAGCTGGGAGGAA 894
 Qy 237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256
 Db 895 ATGCTGAATAAGCGAAGTTGGCCATGGGTACATGGACCGGCCCTTGGCTCAACCCAGCC 954
 Qy 257 AspLeuHisCysProProSerAlaProAsnHisSerArgGlnAlaProAsnValAla 276
 Db 955 GACCCAGATTGCCCTGCCACAGCCCTTAACAAAAATTCAACCAACCTCTTGATGTGCC 1014
 Qy 277 HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTyrGlnGluGlu 296
 Db 1015 CTTGTTTGAATGTGGATGTCAAAGTTTATCCAGGAAGTATATGTCATTTGGCAGGAGGAG 1074
 Qy 297 LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyLeuLeuLeuArgAlaGluAlaLeu 316
 Db 1075 TTGATTGGGTGTACCGTCAAGATGCCATGGAAAATTTGTCACGGCTCAGCCCTG 1134
 Qy 317 GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp 335
 Db 1135 CAACCATGTTCCAGTAAATGACTCCCAAGCAAAATGATGAACACTTCAGGGGCTAGCAC 1194
 Qy 336 TyrGlnThrHisAspIleGlyTyrSerGluGluGlnAlaSerThrValLeuGlnAlaTyr 355
 Db 1195 TATGTCCTCTCAC---ATCAACTGGAATGAAGACAGAGGCGAGCCGCCATCTCTGGAGCCTGG 1251


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Db 3402 GCTCGCTTGGACACATGTTTGGCTCCCGTCTGGACGGTGTGTCCACTCTCGTGG 3461
Qy 1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAla 1092
Db 3462 TGTACTGATGCTTGAGGGTTCGAATTTGATTTCAATTTGTCAGATACTTCTTTGGCGTCT 3521
Qy 1092 uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112
Db 3522 GGCCATTCTACCGCTTTGGGGTTCTCAATGGACTGGTCTGTGCTGCTGCTTCTTATC 3581
Qy 1112 rLeuLeuGlyProProGluValIle-----GlnMetTyrLysG1 1126
Db 3582 CTTCTTTGGACCGTGTCTCGAGGTCTCTCCAGCAATGGCTAAACCGACTGCCACTCC 3641
Qy 1126 uSerProGluLeuLeuSerProPro-----AlaProGlnGlyGlyLe 1141
Db 3642 TTCGCTGAG-----CGCCTCCAGTGTCTCGGGTTTCCGCTGCTCGTCTGCACAC 3695
Qy 1141 uArgTyrGlyAlaSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
Db 3696 GAACAATGGGTCTGATTCCTCGACTCGAGTACAGCTCTCAGACCAGGTGTCTGCAT 3755
Qy 1159 ----- 1159
Db 3756 CAGTGAGAGCTCAGCAATACGAAGCACAGCAGGGTGCAGGGCCCTGCCACCAAGT 3815
Qy 1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro----Al 1177
Db 3816 GATTGTGAAGCCACAGAAACCTGTCTTTGCCGGTGCACATGTGTGCTCATCGGACTC 3875
Qy 1177 aProAspGluProProTrpSerProAlaAla-----ThrSerGlyAsnLeuSe 1194
Db 3876 CAGACATCAGCCCTCCCTGACCCTCGGCAACAGCCACCCCTCGACTCTGGCTCCCTGTC 3935
Qy 1194 rSerArgGlyProGly 1199
Db 3936 C-----CCTGGA 3942

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RESULT 10

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US-09-754-032-3
; Sequence 3, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
;              GOODRICH, LISA V
;              JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-754-032-3

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Alignment Scores:
Pred. No.: 6,28e-303 Length: 5187
Score: 3337.00 Matches: 677
Percent Similarity: 69.59% Conservative: 204
Best Local Similarity: 53.48% Mismatches: 306
Query Match: 53.20% Indels: 80
DB: 10 Gaps: 20

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US-09-990-046-2 (1-1203) x US-09-754-032-3 (1-5187)

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Qy 3 ArgSerProLeuArgGluLeu-----ProProSerTyrThrProProAlaArgThr 20
Db 178 CGGCGCGCGCGGACCGGGACTATCTGCACCGGCCAGCTACTGC---GAGCGCGCCTTC 234
Qy 21 AlaAlaProGlnLeuAlaGlySerLeu-----LysAlaProLeuTrpLeuArg 37
Db 235 GCTCTGGAGCAGATTTCRAAGGGAGGCTACTGGCCGGAAGCGCCGCTGTGCTCAGA 294
Qy 38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
Db 295 GCAGAGTTTCAGAGACTCTATTATAACTGGGTGTACATTCAAAGAACTCGGCAAG 354
Qy 58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77
Db 355 TTTTGGTGTGGGTCTCTCATATTGGGGCCCTTCGCTGTGGGATTAAGAGCAGCTAAT 414
Qy 78 IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu 97
Db 415 CTCGAGACCAACGTCGAGGAGCTGTGGGTGGAGTTGGTGGAGCTGAGTCAGATAATTA 474
Qy 98 HisTyrThrLysGluLysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGln 117
Db 475 AATTATACCCGTCAAGATAGAGAGAGGCTATGTTTAATCCTCAACTCATGATACAG 534
Qy 118 ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisGln 137
Db 535 ACTCCAAAGAAAGAGGCGCTAATGTTCTGCACACAGAGGCTCTCTCGCAACACCTGGAC 594
Qy 138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn 157
Db 595 TCAGCACTCCAGCCAGTCGTGTGCACGCTCTACATGTATACAGCAATGGAAGTGGAA 654
Qy 158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleLtrpMetIle 177
Db 655 CATTTGTCTACAAATCAGGGGAACCTTATACGGAGACAGGTTTACATGATCAGATAATA 714
Qy 178 GluLysLeuPheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197
Db 715 GAATACCTTTACCTTGTCTTAATCATTAACCTTTGGACTGCTTCTGGGAAGGGCAAG 774
Qy 198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217
Db 775 CTACAGTCCGGGACAGCATACCTCTAGTGAAGCCTCTTACGTTGACAACTTTTCAC 834
Qy 218 ProGluGlnLeuLeuGluGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236
Db 835 CCCTTGGAAATTCCTAGAAGAGTTAAAGAAATAAATACTACCAAGTGGACAGCTGGAGAA 894
Qy 237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256
Db 895 ATGCTGAATAAGCCGAAGTTGGCCATGGGTGATATGACCGCGCTTGCCTCAACCCAGCC 954

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Qy	158	LysileCysTyrLysSerGlyValProLeuileGluAsnGlyMetileGluTrpMetile	177	Qy	514	LeuMetalalaLeuValProileProAlaLeuArgAlaPheSerleuGlnAlaile	533
Db	655	CATTGTGTCTACAAATCAGGGAACTTATCAGGAGACAGAGTTATCATGGATCAGATAATA	714	Db	1732	TTATGGCGCGCATTCATCCTATCCTCCCTCGCAGGCTTCCTCCCTCCAGGCTGCTG	1791
Qy	178	GluLysLeuPheProCysValileLeuThrProLeuAspCysPheTrpGluGlyAlaLys	197	Qy	534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaileLeuSerLeuAsp	553
Db	715	GAATACCTTTACCTTGTCTTAATCATTCACCTTTGGACTGCTTTGGGAGGGGCAAG	774	Db	1792	GTGGTGGTATTCAATTTTGGCTATGGTTCTGTCTCATTTTCTCGCAATTCCTCAGCATGAT	1851
Qy	198	LeuGlnGlySerAlaTyrLeuProGlyArgProAspileGlnTrpThrAsnLeuAsp	217	Qy	554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer	573
Db	775	CTACAGTCGGGACAGCATACCTCTAGTAGGCTCTCTTACGGTGGGCAAACTTTGAC	834	Db	1852	TTATACAGAGCTGAGACAGAGATGGATATTTCTGCTGTTTTCACAGCCCTGTGTGC	1911
Qy	218	ProGlnGlnLeuLeuGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu	236	Qy	574	AlaGlnValileGlnLeuProGlnGluLeuGlyAspGlyThrValProValGlyL	593
Db	835	CCCTTGAATTCCTAGAAGATTAAAGAAATAAACTACCAAGTGGACAGCTGGGAGAA	894	Db	1912	AGCAGGCTGATTCAAGTTGAGCCACAGGCTTACACAGAGCCTCACAGTAACCCCGGTAC	1971
Qy	237	LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp	256	Qy	593	eala-----HisLeuThrAlaThrValGln-----	601
Db	895	ATGCTGAATAAAGCCGAAGTTGGCCATGGGTATCATGGACCGGCTTGCCTCAACCCAGCC	954	Db	1972	AGCCCCCCCCCATACACAGCCACAGCTTCGCCCCACGAAACCATATCATATGCGAG	2031
Qy	257	AspLeuHisCysProProSerAlaProAsnHisSerArgGlnAlaProAsnValAla	276	Qy	602	---AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db	955	GACCCAGATTGCCCTGCCACAGCCCTTACAAAATTCACCAAACTCTTGATGTGCC	1014	Db	2032	TCACCGTTTCAGTCCGACAGAGTATGACCTTCACAGCAGCTGTACTACACCCGCC	2091
Qy	277	HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu	296	Qy	620	nAlaHis-----LeuValProProProSerAspProLeuGlySe	633
Db	1015	CTTGTGTTGAATGGTGGATGTCAGGTGTTTATCCAGGAAGTATATGCTTGGCAGGAG	1074	Db	2092	GAGCCACGCTCTGAGATCTGTACAGCCTGTTCACCGTCCACCCAG-GACAACTCAGCTG	2150
Qy	297	LeuLeuGlyGlyMetAlaArgAspProGlnGlyLeuLeuLeuArgAlaGluAlaLeu	316	Qy	633	rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThrAr	653
Db	1075	TTGATTGTGGTGGTACCGTCAAGATGCCACATGGAAATCTGTACAGGCTCAGCCCTG	1134	Db	2151	TCAGAGTCCGAGAGCAGCAGCTCTACCGGGACCTGCTCTCCAGTTCAGACTCC--	2208
Qy	317	GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp	335	Qy	653	gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr	673
Db	1135	CAACCATGTTCCAGTTAATGACTCCCAAGCAATATGTAACACTTCAGGGGTACGAC	1194	Db	2209	---AGCTCCACTGCTCGAGCCCTCGACCAAGTGGACACTCTCTCTGTTTGAGA	2264
Qy	336	TyrGlnThrHisAspileGlyTrpSerGluGluAlaSerThrValLeuGlnAlaTrp	355	Qy	673	gTyrGlnPheAlaProLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh	693
Db	1195	TATGCTCTCAC---ATCACTGGAATGAAGACAGGCGAGCCATCTCTGGAGGCTGG	1251	Db	2265	GAAGCACTATGCTCTTCTCTGAAACCCCAAGCAAGGTTGTGTATCTCTCTTTT	2324
Qy	356	GlnArgArgPheValGlnLeuAlaGlnAlaLeuProGluAsnAlaSerGlnGlnile	375	Qy	693	eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe	713
Db	1252	CAGAGGACTTACGTGGAGTGGTTCATCAAGTGTGCCCCCAAACTCCACTCAAAAGTG	1311	Db	2325	CCTGGCTTGTGGGGTTCAGCTTTATGGACCCCGAGTGGAGACGGGCTGGACCT	2384
Qy	376	HisAlaPheSerSerThrLeuAspAspileLeuHisAlaPheSerGluValSerAla	395	Qy	713	uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy	733
Db	1312	CTTCCCTTCACACCCAGCCCTGGACGACATCTTAAATCCTTCTCTGATGTCAGTGTC	1371	Db	2385	CACGGACATGTTCCCGGGGAACACAGAGAATATGACTTCATAGCTGCCAGTTCAAGTA	2444
Qy	396	AlaArgValValGlyGlyLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg	415	Qy	733	rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerG1	753
Db	1372	ATCCGAGTGGCCAGCGGCTACTACTGATGCTTGCCTATGCTGTTTAAACCATGTCGC	1431	Db	2445	CTTCTCTTTCACCAATGTATATAGTACCCAGAAAGCA---GACTACCCGAATATCCA	2501
Qy	416	TrpAspCysAlaGlnSerGlnLysSerValGlyLeuAlaGlyValLeuValAlaLeu	435	Qy	753	nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr	773
Db	1432	TGGGACTGCTCAAGTCCAGGAGTCCGCTGGGCTGGCTGGCTGCTGTTGGTGGCTG	1491	Db	2502	GCACCTACTTTCAGACCTTCATAAGAGTTTCAGCAATGTGAGTATGTCATGCTGGAGA	2561
Qy	436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr	455	Qy	773	oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleG1	793
Db	1492	TCAGTGGCTGACAGATTGGGCTCTGCTCTGTTGATGTCATTTTAAATGTCGAC	1551	Db	2562	GAACAGCACTTCCCCAAATGTGGCTGCTACTTTAGAGACTGGCTTCAAGGACTTCA	2621
Qy	456	ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAla	475	Qy	793	nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnG1	813
Db	1552	ACTCAGGTTTTCGCGTTTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1611	Db	2622	GGATCATTTGACAGTGTGCGGAACTGGGAGGATCATGCCAAATTAATAAATGG	2681
Qy	476	HisAlaPheThrGluAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGlu	493	Qy	813	ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr	833
Db	1612	CATGCATTGAGTGAACACAGACAGATAAGAGATTCCATTTGAGGACAGGACTGGGAG	1671	Db	2682	ATCAGATCAGCGGGTCTTCGTTTACAACTCCTGGTGAGACTGSCAGCCGAGACAAGCC	2741
Qy	494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe	513	Qy	833	oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr	853
Db	1672	TGCTCAAGGCGACCGGACCGCTGGCCCTCACCTCCATCAGCAATGTCACCGCTTC	1731	Db	2742	CATCGACATTAGTTCAGTTGACTTAAACAGCGCTGTGGTAGCAGGATGGCATTAATCC	2801
				Qy	853	oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl	873

2802 GAGCGCTTTCTACATCTACCTACCGCTGGGTCAGCAACGACCTGTAGCTTACGCTGC 2861

873 aSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspIysTyrAspThrThr 893

2862 CTCCTCCAGGCCAATCTCCGGCTTACCGCGCGAGTGGGTCCATGACAAAGCCGACTACAT 2921

893 rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912

2922 GCCAGAGACCGGCTGAGATCCAGCAGCAGAGCCCATCAGGTACGCTCAGTTCCTCTT 2981

912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932

2982 CTACTCTAACCGCTTACGACACCTCTAGACTTTGTGAGGCCATAGAAAAGTGAGAGT 3041

932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952

3042 CATCTGTAAACACTATACGACCTGGGACTGTCAGCTACCCCAATGGCTACCCCTTCCT 3101

952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972

3102 GTTCTGGAGCAATACATACGCTGGCCACTGCGCACTGCTGCTATATCCATCAGCGTGTGCT 3161

972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuI 992

3162 GGCCTGCACGTTCTAGTGTGCGAGTCTTCTCTGAACCCCTGGACGCGCGGATCAT 3221

992 eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyI 1012

3222 TGTATGGTCTGCTGTATGACCGTTGAGCTCTTTGGCATGATGGGCTCATTTGGGAT 3281

1012 eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh 1032

3282 CAAGCTCAGTGCTGTGCTGTGTCATCTCTGATTGCATCTGTGGCATCGGAGTGAGTT 3341

1032 eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052

3342 CACGCTCCAGTGGCTTTGGCTTTCTCGACAGCATTTGGGACACCAACACAGGCTAT 3401

1052 aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGl 1072

3402 GCTCGCTCTGACACACATGTTGCTCCGTTCTGGACGGTGTGTGTCACATCTCGCTGG 3461

1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092

3462 TGTACTCATGCTTGCAGGGTCCGAATTGATTTCATTGTGCAGACTCTTTGCGCGTCT 3521

1092 uThrValLeuLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112

3522 GGCCATCTCACCGTCTGGGGTCTCAATGAGTGTGTTCTGCTGCTGCTCTCTTATC 3581

1112 rIleLeuGlyProProGluValIle-----GlnMetTyrLysGl 1126

3582 CTTCTTTGGACCGTGCTCTGAGGTCTCCAGCAATGGCTTAACCCAGCTGCCCACTCC 3641

1126 uSerProGluIleLeuSerProPro-----AlaProGlnGlyGlyGlyLe 1141

3642 TTGCGCTGAG-----CCGCTCCAAAGTGTGCTCGGTTTGGCGGCTCTCTGGTCACAC 3695

1141 uArgTTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159

3696 GAACAATGGGTCTGATTCTCCGATCTCGAGTACAGCTCTCAGACACGGTGTCTGGCAT 3755

1159 ----- 1159

3756 CAGTGAGGAGCTCAGGCANTACGAAGCACAGCAGGTTGCGGAGGCCCTGCCCAACCAAGT 3815

1160 ----MetThrValAlaIleHisProProLeuProGlyAlaTyrIleHisPro---Al 1177

3816 GATTGTGGAAGCCACAGAAACCCCTGTCTTTGCCCGGTCCACTGTGGTTCATCCGACTC 3875

1177 aProAspGluProProTrpSerProAlaAla-----ThrSerSerGlyAsnLeuSe 1194

1194 ----- 1194

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Db      3876 CAGACATCAGCCTCCCTTGAGCCCTCGGAAACAGCCCACTGACTCTGGCTCCITGTC 3933
Qy      1194 rSerArgGlyProGly 1199
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      |||||
Db      3936 C-----CCTGGA 3942

RESULT 12
US-10-421-446-3
; Sequence 3, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
;              GOODRICH, LISA V
;              JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-421-446-3

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Alignment Scores:	
Pred. No.:	6.28e-303
Score:	3330.00
Percent Similarity:	69.59%
Best Local Similarity:	53.48%
Query Match:	53.20%
DB:	15
	20
	Gaps:
	80
	Indels:
	90
	Mismatches:
	306
	Conservative:
	204
	Matches:
	677
	Length:
	5187

US-09-990-046-2 (1-1203) x US-10-421-446-3 (1-5187)

Qy	3	ArgSerProProLeuArgGluLeu-----ProProSerTyrThrProProAlaArgThr	20
Db	178	CGCGCGCGCGCGACGGGACTATCTACGCGGCCAGCTACTGC---GACGCGCGCTTC	234
Qy	21	AlaAlaProGlnIleLeuAlaGlySerLeu-----LysAlaProLeuTrpLeuArg	37
Db	235	GCTCTGGAGCAGATTTCACGGGGAAGGCTACTGGCGGAACGCGGCTGTGGCTGACA	294

Db 2445 CTTCTCTTTCTACAAACATATATATAGTACCCAGAAAGCA---GACTACCCGAATATCCA 2501
 QY 753 nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773
 Db 2502 GCACCTACTTTACGACCTTCATAAGAGTTTCAGCAATGTGAAGTATGTCTCATCTGGAGGA 2561
 QY 773 oAlaThrGlnAlaProArgThrTIPLeuHisTyrTyrArgAsnTrpLeuGlnGlyLeu 793
 Db 2562 GAACAAGCAACTTCCCAAAATGTGGCTGCACTACTTTAGAGACTGGCTTCAAGGACTTCA 2621
 QY 793 nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnG 813
 Db 2622 GGATGCATTTTCAGACGTGATCGGAACTGGAGGATCATGCCAAACAAATTATATAAATGG 2681
 QY 813 ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr 833
 Db 2682 ATCAGATGACGGGGTCTTCGCTTACAACTCCTGTGCAGACTGGCAGCCGAGACAAGCC 2741
 QY 833 oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr 853
 Db 2742 CATGCATATTAGTCAGTTGACTAAACACAGCGTCTGGTAGACGACATGGCATTTAATCC 2801
 QY 853 oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl 873
 Db 2802 GAGCGCTTTTACATCTACCTGACCGCTGGGTGAGCAACAGCCCTGTGTAGCTTACGCTGC 2861
 QY 873 aSerGlnAlaAsnPheTyrProProGluTrpLeuHisAspLysTyrAspThrTh 893
 Db 2862 CTCCAGCCCAACATCCGGCTCACCGCGCGAGTGGGTCTCATGACAAAGCCGACTACAT 2921
 QY 893 rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
 Db 2922 GCCAGACACCGGCTGAGATCCAGCAGCAGACCCATCGAGTACGCTCAGTTCCTTT 2981
 QY 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
 Db 2982 CTACCTCAACGGCTACGAGACACCTCAGACTTTGTGGAAGCCATAGAAAAGTGAGAGT 3041
 QY 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
 Db 3042 CATCTGTAACTATACGAGCGCTGGAGCTGCAGCTACCCCAATGGCTACCCCTTCT 3101
 QY 952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
 Db 3102 GTTCTGGAGCAATACATCAGCTGCGCCACTGGCTGCTATCCATCAGCGTGGTGT 3161
 QY 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuLeuLeuLeuLeuAlaGlyLeuI 992
 Db 3162 GGCCTGCAGCTTTCTAGTGTGGCAGCTTCTCCTCTGAACCCCTGGACGCGCGGATCAT 3221
 QY 992 eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyI 1012
 Db 3222 TGTATGTGCTCTGCTGTGATGACCTTGAGCTCTTTGGCATGGGCTCATTTGGAT 3281
 QY 1012 eLysLeuSerAlaIleProValValLeuLeuValAlaSerValGlyIleGlyValGluPh 1032
 Db 3282 CAAGCTGAGTGTGTGCTGTGCTATCCTGATCTGTGTGCTGCGAGTGGAGTT 3341
 QY 1032 eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052
 Db 3342 CACCGTCCAGTGGCTTTGGCTTTCTGACAGCCATTGGGAGCAAGAACACAGGGCTAT 3401
 QY 1052 aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuG 1072
 Db 3402 GCTGCTCTGGACACATGTTGCTCCCGTTCGACGCTGCTGTGCTCACTCTGCTGG 3461
 QY 1072 yLeuLeuMetLeuAlaGlySerHisPheIleValArgTyrPhePheAlaAlaLe 1092
 Db 3462 TGTACTGATGCTGCGAGGTCGGAATTTGATTTCACTTCAGATACCTTTTGGCGTCT 3521
 QY 1092 uThrValLeuThrLeuLeuGlyLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112

Db 3522 GGCATTTCTCACCGCTTTGGGGTTCTCAATGCACTGGTTCTGCTGCTGCTCTTATC 3581
 QY 1112 rIleLeuGlyProProGluValIle-----GlnMetTyrIlysG 1126
 Db 3582 CTTCTTTGGACGCTGCTCTGAGGTCTCCAGCAATGGCTTAAACCGCACTGCCCACTCC 3641
 QY 1126 uSerProGluLeuLeuSerProPro-----AlaProGlnGlyGlyLe 1141
 Db 3642 TTGCGCTCAG-----CCGCTCCCAAGTGTCTCGGTTTCCGCTGCTCTGGTCAAC 3695
 QY 1141 uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
 Db 3696 GAACAATGGGTCTGATTCCTCCGACTCGAGTACAGCTCTCAGACCACTGCTGGCAT 3755
 QY 1159 ----- 1159
 Db 3756 CAGTGAGGAGCTCAGGCAATACGAGGACACAGCGGTGCGGAGCCCTGCCCAAGT 3815
 QY 1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro---Al 1177
 Db 3816 GATTTGGAGCCACAGAAAACCTGTCTTTTGGCCGCTCCACTGTGTCTATCCGACTC 3875
 QY 1177 aProAspGluProProTrpSerProAlaAla-----ThrSerSerGlyAsnLeuSe 1194
 Db 3876 CAGATCAGCTCCCTTGTGACCCCTCGGCAACAGCCCACTGCGACTCTGCTGCTCTGTC 3935
 QY 1194 rSerArgGlyProGly 1199
 Db 3936 C-----CCTGGA 3942

RESULT 13

US-10-421-446-9
 ; Sequence 9, Application US/10421446
 ; Publication No. US20030186309A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; GOODRICH, LISA V
 ; JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/421,446
 ; FILING DATE: 22-Apr-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/724,631
 ; FILING DATE: 28-Nov-2003
 ; APPLICATION NUMBER: US/08/656,055
 ; FILING DATE: 1996-05-31
 ; APPLICATION NUMBER: 08/540,406
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5187 base pairs

QY	277	HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu	296
Db	1015	CTTGTTTGAATGGTGGATGTCAGAGTTTATCCAGGAAGTATATCATTTGGCAGGAGG	1074
QY	297	LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuArgAlaGluAlaLeu	316
Db	1075	TTGATTGGTGGTACCGTCAGAAATGCCATCGAAACTTGTGAGCCCTCAGCCCTG	1134
QY	317	GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly	335
Db	1135	CAAAACCATGTTCCAGTTAATGACTCCCAAGCAATGTATGAACACTTCAGGGGCTACGAC	1194
QY	336	TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp	355
Db	1195	TATGTCCTCAC--ATCAACTGGAATGAAGACAGGCGCAGCCCTCTCGAGGCTGG	1251
QY	356	GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle	375
Db	1252	CAGAGGACTTACGTGGAGGTGTTCTCAAGAGTGTGCGCCCAAACTCCACTCAAAAGGTG	1311
QY	376	HisAlaPheSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla	395
Db	1312	CTTCCCTTCAACACACGACCCCTGGACGACATCTTAAATCTCTCTGATGTCAGTGTC	1371
QY	396	AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg	415
Db	1372	ATCCGAGTGCCACGCGCTACTTACTGATGCTTGCCTATGCTGCTTAAACATGCTGCGC	1431
QY	416	TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu	435
Db	1432	TGGGACTGCTCCAAAGTCCCGAGGTGCGTGGGCTGGCTGGCTGCTGTTGGTGGCTG	1491
QY	436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr	455
Db	1492	TCAGTGGCTCCAGAGTGGCCCTCTGCTCTGATGTCATTTCTTTAATGCTGCGACA	1551
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Db	1552	ACTCAGGTTTGGCGTTCTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1611
QY	476	HisAlaPheThrGluAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGlu	493
Db	1612	CATGCATTCAGTGAACACGACGACGAATAAGAGGATTCATTTGAGGACGAGGCTGGGAG	1671
QY	494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe	513
Db	1672	TGCCTCAAGCCACCGGACGCGTGGCCCTCACCTCCATCACAATGTCCAGCCCTTC	1731
QY	514	LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle	533
Db	1732	TTTCATGGCGCATTTGATCCCTATCCCTGCGGAGCGTTCTCCCTCCAGGCTGCTGTG	1791
QY	534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp	553
Db	1792	GTGGTGATTCATTTTGTCTGCTCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1851
QY	554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer	573
Db	1852	TTATACAGCTGAGGACAGAGATTTGATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCT	1911
QY	574	AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIle	593
Db	1912	AGCAGGGTGAATCAAGTTGAGCCCTACAGAGCTTACAGAGCTTCAAGTAAACCCGGTAC	1971
QY	593	ValAla-----HisLeuThrAlaThrValGln-----	601
Db	1972	AGCCCCCACCCTCATACAGGACGACGCTCGCCCAAGAAACCATATCATCTATGCGAG	2031
QY	602	-----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db	2032	TCCACCGTTACCTCGGACAGAGTATGACCTCTACACGACGCTGTACTACACCCGCGC	2091
QY	620	nAlaHis-----LeuValProProSerAspProLeuGlySe	633

QY	277	HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu	296
Db	1015	CTTGTTTGAATGGTGGATGTCAGAGTTTATCCAGGAAGTATATCATTTGGCAGGAGG	1074
QY	297	LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuArgAlaGluAlaLeu	316
Db	1075	TTGATTGGTGGTACCGTCAGAAATGCCATCGAAACTTGTGAGCCCTCAGCCCTG	1134
QY	317	GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly	335
Db	1135	CAAAACCATGTTCCAGTTAATGACTCCCAAGCAATGTATGAACACTTCAGGGGCTACGAC	1194
QY	336	TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp	355
Db	1195	TATGTCCTCAC--ATCAACTGGAATGAAGACAGGCGCAGCCCTCTCGAGGCTGG	1251
QY	356	GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle	375
Db	1252	CAGAGGACTTACGTGGAGGTGTTCTCAAGAGTGTGCGCCCAAACTCCACTCAAAAGGTG	1311
QY	376	HisAlaPheSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla	395
Db	1312	CTTCCCTTCAACACACGACCCCTGGACGACATCTTAAATCTCTCTGATGTCAGTGTC	1371
QY	396	AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg	415
Db	1372	ATCCGAGTGCCACGCGCTACTTACTGATGCTTGCCTATGCTGCTTAAACATGCTGCGC	1431
QY	416	TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu	435
Db	1432	TGGGACTGCTCCAAAGTCCCGAGGTGCGTGGGCTGGCTGGCTGCTGTTGGTGGCTG	1491
QY	436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr	455
Db	1492	TCAGTGGCTCCAGAGTGGCCCTCTGCTCTGATGTCATTTCTTTAATGCTGCGACA	1551
QY	456	ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAla	475
Db	1552	ACTCAGGTTTGGCGTTCTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1611
QY	476	HisAlaPheThrGluAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGlu	493
Db	1612	CATGCATTCAGTGAACACGACGACGAATAAGAGGATTCATTTGAGGACGAGGCTGGGAG	1671
QY	494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe	513
Db	1672	TGCCTCAAGCCACCGGACGCGTGGCCCTCACCTCCATCACAATGTCCAGCCCTTC	1731
QY	514	LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle	533
Db	1732	TTTCATGGCGCATTTGATCCCTATCCCTGCGGAGCGTTCTCCCTCCAGGCTGCTGTG	1791
QY	534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp	553
Db	1792	GTGGTGATTCATTTTGTCTGCTCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1851
QY	554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer	573
Db	1852	TTATACAGCTGAGGACAGAGATTTGATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCT	1911
QY	574	AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIle	593
Db	1912	AGCAGGGTGAATCAAGTTGAGCCCTACAGAGCTTACAGAGCTTCAAGTAAACCCGGTAC	1971
QY	593	ValAla-----HisLeuThrAlaThrValGln-----	601
Db	1972	AGCCCCCACCCTCATACAGGACGACGCTCGCCCAAGAAACCATATCATCTATGCGAG	2031
QY	602	-----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db	2032	TCCACCGTTACCTCGGACAGAGTATGACCTCTACACGACGCTGTACTACACCCGCGC	2091
QY	620	nAlaHis-----LeuValProProSerAspProLeuGlySe	633


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Db 2092 GAGCCACGCTCTGAGATCTCTGACAGCGCTGTACCGTCACCCAG-GACAACTCTAGCTG 2150
QY :|||:|
633 rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlnGluGluThrAr 653
Db :|||:|
2151 TCAGAGTCCGAGACACAGCTCTACAGGAGACCTGCTCTCCCACTCTCTCAGACTCC-- 2208
QY gGlnbysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr 673
Db :|||:|
2209 ----AGCCTCCACTGCTCGAGCCCTCGACCAAGTGGACACTCTCTCGTTTGGCAGA 2264
QY gTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaLeValLeuValLeuPh 693
Db :|||:|
2265 GAAGCACTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2324
QY eGlyAlaLeuLeuGlyLeuSerLeuGlyAlaThrLeuValGlnAspGlyLeuAlaLe 713
Db :|||:|
2325 CTTGGCTTGTGGGGTCAAGCTTTATGGACCAACCGAGTGAGAGACGGCTGGACCT 2384
QY uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy 733
Db :|||:|
2385 CACGACATTTCTCCCGGAAACCCAGAGATATGACTTCTATAGCTGCCAGTTCAAGTA 2444
QY rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl 753
Db :|||:|
2445 CTTCTCTTTCTACAACATGTATATAGTCACCCAGAAAGCA--GACTACCCGATATCCA 2501
QY nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773
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2502 GCACCTACTTTACGACCTTCATAGAGTTTCAGCAATGTGAAGTATGTCATGCTGGAGGA 2561
QY oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyLeGl 793
Db :|||:|
2562 GAACAAGCAACTTCCCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2621
QY nAlaAlaPheAspGlnAspTrpAlaSerGlyArgGileThrArgHisSerTyrArgAsnGl 813
Db :|||:|
2622 GGATGCATTTGACAGTGAAGTGGGAACTGGGAGATCATGCCAAACAAATATAAATGG 2681
QY ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuLeuGlnThrGlyAspAlaGlnGluPr 833
Db :|||:|
2682 ATCAGATGACGGGTCTCTGCTTACAACTCTGCTGGTGCAGCTGGCAGCGCAGCAAGCC 2741
QY oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGluLeuLeuProPr 853
Db :|||:|
2742 CATCGACATTTAGTCAGTTGACTTAAACAGCGTCTGCTGAGCGAGATGGCATCAATATCC 2801
QY oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl 873
Db :|||:|
2802 GAGCGCTTTCTATCTACCTGACCGCTTGGGTGAGCAACGACCCCTGTAGCTTACGCTGC 2861
QY aSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrTh 893
Db :|||:|
2862 CTTCCAGGCCAACATCCCGCCCTCACCGCGCGAGTGGTTCATGACAAAGCGCATCATAC 2921
QY rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db :|||:|
2922 GCCAGAGACCGGCTGAGAACTCCAGCAGCAGCCCATCGAGTACGCTCAGTCTCCCTTT 2981
QY eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db :|||:|
2982 CTACCTCAACGCGCTACGAGACACCTCAGACTTTGTGGAAGCCATAGAAAAGTGGAGGT 3041
QY aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db :|||:|
3042 CATCTGTAAACTATACAGCGCTGGACTGTCACAGTACCCCAATGGCTACCCCTTCT 3101
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Db :|||:|
3102 GTTCTGGAGCAATATACATCAGCTCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 3161
QY uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl 992

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Db 3162 GGCCTGACGTTTCTAGTGTGGCAGTCTTCTCTGAAACCCCTGGACGGCCGGATCAT 3221
QY eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyIl 1012
Db :|||:|
3222 TGTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3281
QY eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh 1032
Db :|||:|
3282 CAAGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3341
QY eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052
Db :|||:|
3342 CACGCTCCAGTGGCTTTGGCTTTCTGACAGCCATTGGGGCAACAAGACACAGGCTAT 3401
QY aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGl 1072
Db :|||:|
3402 GCTGCTCTGGAACACATGTTTGTCTCCGTTCTCGACGGTCTGTGCTGCTGCTGCTGCTG 3461
QY yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092
Db :|||:|
3462 TGTACTGATGCTTGCAGGGTCCGAATTTGATTTTCATTTGTCAGATACTTCTTTGCGCTCT 3521
QY uThrValLeuThrLeuLeuGlyLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112
Db :|||:|
3522 GGCAATTTCTCACCGTCTTGGGGTCTCTCAATGGACTGGTTCTGCTGCTGCTGCTGCTGCT 3581
QY rLleLeuGlyProProGluValIle-----GlnMetTyrLysGl 1126
Db :|||:|
3582 CTTCTTTGACCGTCTGCTGAGGTGTCTCCAGCAATGGCTTAAACGACTGCCACTCC 3641
QY uSerProGluLeuLeuSerProPro-----AlaProGlnGlyGlyLe 1141
Db :|||:|
3642 TTGCGCTGAG-----CCGCTCCAAAGTGTGTCGCGTTTGGCGTCTGCTGCTGCTGCTGCT 3695
QY uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
Db :|||:|
3696 GAACAATGGTCTGATTTCTCCGACTCGGAGTACAGCTCTCAGACCAACGCTGCTGCTGCT 3755
QY 1159 ----- 1159
Db :|||:|
3756 CAGTGAGGAGCTCAGCAATACAGACACAGCGGTGCGGAGGCGCTGCCACCAAGT 3815
QY 1160 ----MetThrValAlaIleHisProProProProGlyAlaTyrIleHisPro---Al 1177
Db :|||:|
3816 GATTGTGGAAGCCACAGAAAACCTGTCTTTGCGCGTCCACTGTGTGCTCATCCGACTC 3875
QY 1177 aProAspGluProProTrpSerProAlaAla-----ThrSerSerGlyAsnLeuSe 1194
Db :|||:|
3876 CAGACATCAGCTCCCTTGCACCCCTGGCAACAGCCCACTGGACTCTGCTGCTGCTGCTGCT 3935
QY 1194 rSerArgGlyProGly 1199
Db :|||:|
3936 C-----CCTGGA 3942

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RESULT 14

US-10-302-279-1

; Sequence 1, Application US/10302279

; Publication No. US20030171566A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Michael Carlton

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; TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene

; NUMBER OF SEQUENCES: 84

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

Sun Nov 28 09:38:32 2004

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

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FEATURE:
NAME/KEY: CDS
LOCATION: 442..4332
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-302-279-1

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Alignment Scores:		
Pred. No.:	1.1e-302	Length: 6568
Score:	3346.00	Matches: 684
Percent Similarity:	65.63%	Conservative: 205
Best Local Similarity:	50.15%	Mismatches: 273
Query Match:	53.19%	Indels: 182
Da:	15	Gaps: 17

US-09-990-046-2 (1-1203) x US-10-302-279-1 (1-6568)

31	LysAlaProLeuTrpLeuA: gAlaTyPheGlnGlyLeuLeuPheSerLeuGlyCysGly	50
208	AAAGCGCGCTGTGGCTGAGAGCGAAGCTTTTATTTAAACTGGGTGTTTAC	267
51	IleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAla	70
268	ATTCAAAAAAATCGGCAAGTCTTGTTGTTGGGGCTCTCTATATTGGGGCTTCGGC	327
71	LeuGlyLeuArgMetAlaIleLeuGlyThrAsnLeuGlnLeuTrpValGluValGly	90
328	GTGGGATTTAAAGCAGCGCAACTCGAGACCAACTGGAGAGCTGTGGTGTGAAGTTGA	387

[illegible]

Db	2536	GACTGGCTTCAGGACATTCAGGATGCATTGTGACAGTGCATGGGAAACCGGAAAAATCATG	2595
Qy	807	ArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuLeuGln	826
Db	2596	CAAACAATTAACAGATGATACAGCATGAGTCCCTTGCTCAAACTCCTGGTCAA	2655
Qy	827	ThrGlyAspAlaGlnclupProLeuAspPheSerGlnLeuThrThrArgLysLeuValAsp	846
Db	2656	ACCGGAGCGCGATAAGCCCATGCATCAGCCAGTTGACTAAACAGCGTCTGGTGGAT	2715
Qy	847	ArgGluGlyLeuLeuProProGluLeuPheTyrMetGlyLeuThrValTnpValSerSer	866
Db	2716	GCAGATGGCATCAATTAATCCAGCGCTTTTACATCTACCTGACGGTGTGGGTGAGCAAC	2775
Qy	867	AspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGluThrLeu	886
Db	2776	GACCCCGTCGGTATGCTGCCCTCCAGGCCAACTCCGGCCACACCGACAGAAATGGGT	2835
Qy	887	HisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnProLeu	905
Db	2836	CACGACAAAGCGCATACATGCCTGAAACAGGCTGAGAAATCCCGGCAGCAGAGCCCATC	2895
Qy	906	GluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGlu	925
Db	2896	GAGTATGCCAGTTCCTCTTCTCAACGGCTTGGGGACACCTCAGACTTTGTGGAG	2955
Qy	926	AlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyr	945
Db	2956	GCAATTGAAAAGTAAGGACCATCTGCAGCACTATACGAGCCTGGGGCTGTCCAGTTAC	3015
Qy	946	ProSerGlySerProPheLeuPheTnpGluGlnTyrLeuGlyLeuArgArgCysPheLeu	965
Db	3016	CCCAACGGCTACCCCTTCTCTCTGGAGCAGTACATCGCGCTCCGCCACTGGCTGCTG	3075
Qy	966	LeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsn	985
Db	3076	CTGTTCAACGGTGGTGTGGCGTCGCACATCTCTGTGCGCTGTCTTCTCTCTGAAC	3135
Qy	986	ProTnpAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGly	1005
Db	3136	CCCTGGACGGCGGATCATTTGATGGTCTCGCGCTGATGACGTCGAGCTGTTTCGGC	3195
Qy	1006	IleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSer	1025
Db	3196	ATGATGGCCCTCATCGAATCAAGCTCAGTCCCGTCCCGTGGTCATCTCTGATCGCTCT	3255
Qy	1026	ValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGlnGly	1045
Db	3256	GTTGGCATAGAGTGAGTTCACCGTTCAGTGTCTTGGCCCTTCTGACGGCCCATCAGC	3315
Qy	1046	SerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGly	1065
Db	3316	GACAAAGACCGCAGGCTGTGCTTGCCTGGAGCACATGTTTGGACCCGTCTGGATGGC	3375
Qy	1066	AlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleVal	1085
Db	3376	GCGGTGTCCACTCTGCTGGAGTGTGATGCTGGCGGATCTGAGTCTCGACTTCATCTGC	3435
Qy	1086	ArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuVal	1105
Db	3436	AGGTATTTCTTGCTGTGTGGACATCTCCACATCTCCGCGTGTCTCAATGGGTGTTT	3495
Qy	1106	LeuLeuProValLeuLeuSerIleLeuGlyProProGluVal-	1120
Db	3496	TTGCTTCCCGTGTGTTTGTCTTCTTGGACCATATCTTGAGGTGTCTCCAGCCACGGC	3555
Qy	1120	-----	1120
Db	3556	TTGAACCGCTGCCACACCCCTCCCTGAGCCACCCCCCGCGTGGTCCGCTTCGCCCATG	3615
Qy	1120	-----	1120
Db	3616	CCGCCCGGCCACAGCACAGCGGGTCTGATTCCTCCGACTCGAGTAGTATTCGCCAGCG	3675

Db 1225 CAGAACTCCACTCAAAAGGTGCTTTCTTACCACACGACCCCTGGACGACATCTCTGAAA 1284
QY 389 AlapheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyr 408
Db 1285 TCCTTCTCTGAGCTCAGTGTCTATCGCGTGGCCAGCGGTACTTACTCATGTCTCGCTAT 1344
QY 409 AlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeuAla 428
Db 1345 GCCTGTCTAAACCATCTCGCTGGGACTGTCTCAAGTCCACGGTGGCGTGGGGTGGCT 1404
QY 429 GlyValLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGly 448
Db 1405 GCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1464
QY 449 IleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyLeuVal 468
Db 1465 ATTTCTTTAACGCTGCAACAACTCAGGTTTGGCTTCTGCTCTTGGTGTGGTGTG 1524
QY 469 AspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly-----ThrPro 486
Db 1525 GATGATGTTTCTTCTGCGCCACGCTTCAAGTGAACACGACGACAGAAATAAAGATCCCT 1584
QY 487 LeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyThrSerValValLeuThrSer 506
Db 1585 TTTGAGGACAGGACCGGGAGTGTGCTGAAGCGCACAGGAGCCAGCGTGGCCCTCACGTCC 1644
QY 507 IleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeuArgAla 526
Db 1645 ATCAGCAATGTCACAGCTTCTTTCATGGCCGCTTAATCCCAATTCGCGCTCTCGGGCG 1704
QY 527 PheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeuValPhe 546
Db 1705 TTCTCCCTCCAGGACGGGTAGTAGTGTCAATTTTGCATGGTTCCTCATTTT 1764
QY 547 ProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspValLeuCys 566
Db 1765 CTGTCAATTCACAGTGGATTATATCGACGCGAGGACAGGACTGGATATTTCTGC 1824
QY 567 CysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeuGlyAsp 586
Db 1825 TGTTTTACAAGCCCTGCGTCACAGAGTATTCAGTTGAACCTCAGGCTCACCGAC 1884
QY 587 -----GlyThrValProValGlyIleAlaHis----- 595
Db 1885 ACACAGCAATACCGCTACAGCCGCCACCTCTCCACAGCAGCACACCTTTGCCAT 1944
QY 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSerSer 610
Db 1945 GAAACCGCAGATTACCATGAGTCCACTGTCCAGCTCCGACGAGTACGACCCCCACAG 2004
QY 611 GlnHisValThrIleLeuProProGlnAlaHisLeuValProPro----- 627
Db 2005 CAGGTGTACTACACCCGCTGAGCGCGCTCCGAGATCTCTGTGAGCCCGTCACCGTG 2064
QY 628 ---SerAspProLeuGlySerGluLeuPheSerProGlySerThrArgAspLeuLeu 646
Db 2065 ACACAGGACACCCCTCAGTCCGACGCCAGACCCAGCAGCAGCTCCACAGGACCTGCTC 2124
QY 647 GlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrp 666
Db 2125 TCCAGTCTCCGACTCC-----AGCTCCACTGCTCCGAGCCCGCTGTACGAAGTGG 2178
QY 667 AsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLys 686
Db 2179 ACACCTCATCTTTGCTGAGAGGACNATGCTCTCTTCTTGAACCAAAAGCCCAAG 2238
QY 687 AlaIleValLeuValPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeu 706
Db 2239 GTAGTGGTGTCTTCTTCTGCGCTGTGCGGGGTGAGCTTTATGGCACCCACCGA 2298
QY 707 ValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHisAlaPhe 726
Db 2299 GTGAGAGCGGCTGGACCTTACCGACATTTGACCTCGGGAACACAGAGATATGACTTT 2358

QY 727 LeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGlyGly 746
Db 2359 ATTGTGTGACAAATCAAATACATTTTCTTACACATGATATAGTACCCAGAAAGCA 2418
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QY 767 LysAlaValLeuProProAlaThrGlnAlaProArgThrThrPleuHisTyrTyrArg 786
Db 2476 AAGTATGTATGTGGAAAGAAACAAACAGCTTCCAAATGTGGCTGCCTACTTCTCAGA 2535
QY 787 AsnTrpLeuGlnGlyIleGlnAlaPheAspGlnAspTrpAlaSerGlyArgIleThr 806
Db 2536 GACTGGCTTCAGGACTTCAGATGCATTTGACAGTGACTGGGAACCGGGAATATCATG 2595
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QY 847 ArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTyrValSerSer 866
Db 2716 GCAGATGGCATTAATCCAGCGCTTCTACATCTACCTGACGGTGGGTGAGCAAC 2775
QY 867 AspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrpLeu 886
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QY 887 HisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnProLeu 905
Db 2836 CACGACAAAGCCGACTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2895
QY 906 GluPheAlaGlnPheProPheLeuArgGlyLeuGlnLysThrAlaAspPheValGlu 925
Db 2896 GAGTATGCCAGTCTCCCTTCTACCTCAAGCGCTTGGCGGACACCTCAGACTTTTGGAG 2955
QY 926 AlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyr 945
Db 2956 GCAATTTGAAGAAAGTAAAGGACCATCTGCAGCACTATACGAGCGCTGGGCTGTCCAGT 3015
QY 946 ProSerGlySerProPheLeuPheThrGluGlnTyrLeuGlyLeuArgArgCysPheLeu 965
Db 3016 CCCAAGCGTACCCCTTCTCTTCTGGGAGCAGTACATCGGCTCCGCGCTGCTGCTGCTG 3075
QY 966 LeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsn 985
Db 3076 CTGTTCATCAGCGTGTGTGTGGCTGCATTTCTCTGTGTGTGTGTGTGTGTGTGTGTGT 3135
QY 986 ProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGly 1005
Db 3136 CCTGTGAGCGCGGATCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3195
QY 1006 IleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSer 1025
Db 3196 ATGATGGCGCTCATCGGAATCAGCTCAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 3255
QY 1026 ValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGlnGly 1045
Db 3256 GTTGGCATAGGAGTGGAGTTTCCCGTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3315
QY 1046 SerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGly 1065
Db 3316 GACAAGAACCCGAGCGCTGTGCTTGGCCCTGGAGCACATGTTTGCACCCGCTCTGTGATG 3375
QY 1066 AlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleVal 1085
Db 3376 CCGGTGCTCTGCTGGGAGTGTGATGTGCGGATCTGACTTGCATTCATTCATTCATTC 3435

Sun Nov 28 09:38:32 2004

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Qy 1086 ArgTyrPheAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuVal 1105
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3436 AGGTATTTCTTGCTGTGTCGCAATCCTCACCATCTCGGCGTCTCAATGGCTGGTT 3495
Qy 1106 LeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3496 TTGCTTCCCGTGCTTTGGTCTTTCTTTGGACCATATCTGAGGTGCTCCAGCCACGGC 3555
Qy 1120 ----- 1120
Db 3556 TTGAACGGCTGCCACACCCCTCCCTGTAGCCACCCCGAGCGTGTCTCGCATG 3615
Qy 1120 ----- 1120
Db 3616 CCGCCCGGCACACGACAGCGGTCTGATTCCTCGACTCGGAGTATAGTTCACAGC 3675
Qy 1121 ----- IleInMetTyr ----- 1124
Db 3676 ACAGTGTACGGCTCAGCAGGAGCTTCGGCACTACGAGGCCAGCAGGGCGGGAGGC 3735
Qy 1124 ----- 1124
Db 3736 CCTGCCCAACCAAGTATGCTGGAGCCACAGAAAACCCCTCTTCGCCCACTCCACTGTG 3795
Qy 1125 ----- -LysGluSerProGluIleLeu 1131
Db 3796 GTCCATCCGAAATCCAGGCATCACCCACCTCGAACCAGAAACAGAGCCGCCCTGGAC 3855
Qy 1132 Ser-----ProAlaProGlnGly-----Gly 1139
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3856 TCAGGGTCCCTGCTCCCGACGCGCAGGCCAGCAGCCCGCAGGACCCCGCAGAAA 3915
Qy 1140 GlyLeu----- 1141
Db 3916 GGCTTGTGGCACCCCTCTACAGACCGCGCAGAGAGCTTTTGAAATTTCTACTGAAGG 3975
Qy 1142 -----ArgTrpGly----- 1144
Db 3976 CATTCGGCCCTAGCAATAGGCGCCGCTGGGGCCCTCGCGGGCCGTTCTCAACCCCT 4035
Qy 1145 -----AlaSerSerLeuProGlnSerPheAlaArgValThr 1157
Db 4036 CGGAACCCCAAGTCCACTGCCATGGCGAGCTCCGTGCCCGCTACTGCCAGCCCATCACC 4095
Qy 1158 Thr-----SerMetThrValAlaIleHisProProLeuProGlyAla 1172
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4096 ACTGTGACGGCTTCGTGCTCCGTGACTGTGCGCGTGCACCGCGCGCTGTCCCTGGGCT 4155
Qy 1173 TyrIleHisPro 1176
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4156 GGGCGGAACCCC 4167

```

Search completed: November 22, 2004, 14:19:04
Job time : 1122 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 07:58:15 ; Search time 842 Seconds
(without alignments)

7500.064 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPPIRELPSPSYTPPART.....SPAATSSGNLSSRPGPGPATG 1203

Scoring table:

BLOSUM62
Gapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US0990046/runat_21112004.130919.18522/app_query.fasta_1.1351
-DB=N_Geneseq_23Sep04 -QFMT=fastp -SUFFIX=ring -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0990046 @CGN 1 1 478 @runat_21112004.130919.18522 -NCFU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPHLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6272	100.0	4030	2	AZ31717	Human pat
2	6272	100.0	4030	6	AAD31576	Human pat
3	6272	100.0	4030	8	ABX15923	Human pat
4	6248	99.6	4391	2	AX89478	Human ptc
5	5911	94.2	3453	3	AAA09081	Human pat
6	4682.5	74.7	12886	3	AAA09084	Human pat

ALIGNMENTS

RESULT 1

AZ31717
ID AZ31717 standard; DNA; 4030 BP.

XX AC AZ31717;

XX DT 19-JAN-2000 (first entry)

XX DE Human patched-2 coding sequence.

XX KW Patched-2; ptc-2; human; signalling molecule; hedgehog cascade; stroke; cell proliferation; cell differentiation; testicular cancer; gut disease; degenerative disorder; nervous system disorder; Parkinson's disease; memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia; Huntington's disease; drug addiction; bone disease; skin disease; ulcer; infertility; lung disease; pancreatic disorder; diabetes; osteoporosis; therapy; ss.

XX OS Homo sapiens.

XX PN WO9953058-A1.

XX PD 21-OCT-1999.

XX PF 02-APR-1999; 99WO-US007417.

XX PR 15-APR-1998; 98US-00060939.

XX PA (GETH) GENENTECH INC.

XX

Aaz31728 Human pat
Aad31580 Human pat
Abx15923 Human pat
Aaz31729 Human pat
Aad31581 Human pat
Aax15924 Human pat
Aat14220 Human pat
Aaf64093 Human pat
Aaf32185 Human pat
Aac62839 Human pat
Ade94223 Human ptc
Adh62730 Human pat
Ade48988 Human pat
Aba00374 Human pat
Aav21587 Precis co
Aav21589 Mouse pat
Aav64099 Precis co
Aav64092 Mouse pat
Aaf32177 Butterfly
Aaf32180 Murine pa
Aca62831 Full leng
Aca62834 Mouse pat
Ade94208 Peacock b
Ade94214 Murine pt
Adh62715 Butterfly
Adh62721 Mouse pat
Ade48979 Mouse pat
Ade48973 Butterfly
Aav21590 Human pat
Aav15949 Nevoid ba
Aat14218 Mouse pat
Aba00375 Mouse pat
Aba00376 Butterfly
Abi67232 Thyroid c
Abk84327 Human cdn
Adf81708 Leukaemia
Adf81706 Leukaemia
Aav69382 Human Pat
Abi04551 Drosophil

3955 63.1 4004 2 AAZ31728
3955 63.1 4004 6 AAD31580
3955 63.1 4004 8 ABX15923
3955 54.0 2082 2 AAZ31729
3955 54.0 2082 6 AAD31581
3955 54.0 2082 8 ABX15924
3955 54.0 2082 2 AAT14220
3955 53.4 5288 2 AAV64093
3955 53.4 5288 5 AAF32185
3955 53.4 5288 9 ACA62839
3955 53.4 5288 10 ADE94223
3955 53.4 5288 10 ADH62730
3955 53.4 5288 12 ADE48988
3955 53.4 5288 6 ABA00374
3955 53.2 5187 2 AAV21587
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3955 53.2 5187 5 AAF32177
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3955 53.2 5187 10 ADE94208
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3955 53.2 5288 2 AAV21590
3955 53.2 5288 2 AAV15949
3955 53.2 5187 2 AAT14218
3955 53.1 5187 6 ABA00375
3955 53.1 5187 6 ABA00376
3955 53.1 5187 6 ABI67232
3955 53.1 5187 6 ABK84327
3955 50.6 7753 10 ADF81708
3955 50.6 7753 10 ADF81706
3955 44.6 2032 2 AAV69382
3955 31.9 3861 4 ABL04551

PI De Sauvage FU, Carpenter DA;
XX WPI; 1999-620428/53.
DR P-FSDB; AAY43261.
XX
XX New isolated human patched-2 gene, used to develop products for treating,
PT e.g. cancer and Alzheimer's disease.
XX
XX Claim 1; Fig 1; 124pp; English.
XX
XX This sequence encodes the human patched-2 (ptch-2) protein of the
CC invention. The patched-2 polypeptides are signalling molecules,
CC specifically for signalling and mediator molecules in the hedgehog (hh)
CC cascade which are involved in cell proliferation and differentiation.
CC They can be used for the treatment of disorders which are mediated at
CC least in part by hh, especially Dhh, e.g. testicular cancer. They can
CC also be used for treating degenerative disorders of the nervous system,
CC e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou
CC Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug
CC addiction. Patched-2 agonists can be used to treat gut diseases, bone
CC diseases, skin diseases, diseases of the testis (including infertility),
CC ulcers, lung diseases, diseases of the pancreas, diabetes, and
CC osteoporosis. Antagonists or agonists of patched-2 may be used for
CC treating disorders or creating a desirable physiological condition
CC effected by blocking hh signalling, especially Dhh signalling, e.g.
CC contraception or infertility treatment. The products can also be used for
CC detection, diagnosis, drug screening and production of transgenic animals
XX
XX Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 0 Length: 4030
Score: 6272.00 Matches: 1203
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-990-046-2 (1-1203) x AAZ31717 (1-4030)

QY 1 MetThrArgSerProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db 233 ATGACTGATGCGCGCCCTCAGAGAGCTGCCCGGAGTTACACCCCGAGCTCGAACC 292
QY 21 AlaAlaProGlnLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db 293 GCACACCCAGATCCTAGCTGGAGGCTCGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352
QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db 353 CAGGGCTGCTCTCTCTGGGATGGGATCCAGAGACATTGTGGCAAGTGTCTTT 412
QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleGluThr 80
Db 413 CTGGGACTGTGGCTTGGGGCCCTGGCATAGTCTCCCATGGCCATTATTAGACA 472
QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db 473 AACTTGGACAGCTCTGGGTAGAAGTGGCGAGCGGTGAGCGAGCTGCATTACACC 532
QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db 533 AAGGAGAAGCTGGGGAGAGGCTGCATACACCTCTCAGATGCTGATACAGCCGACGC 592
QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
Db 593 CAGGAGGAGAGAACATCTCTACACCCGAGACATTGGCTCCACCTCCAGGAGCCCTC 652
QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCTGGGATTTGAACAAATCTGC 712
QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180

713 TACAAGTCAGGAGTTCCCTTTATTGAAATCGAATGATTGAGTGGATGATTGAGAGCTG 772
Db
181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyValAlaLysLeuGlnGly 200
QY
773 TTTCCGTGCGGTGATCCCTACCCCTCTGACCTCTTCTGGGAGGAGCAAACTCCAGGG 832
Db
201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
QY
833 GGCTCCGCTACCTGCGCGCGCGCGGATATTCAGTGGACCAACTGGATCCAGAGCAG 892
Db
221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGlyPheArgGluLeuLeuAspLys 240
QY
893 CTGCTGGAGGAGCTGGGTCCCTTTGGCTCCCTTGAGGGCTTCGGGAGCTGTAGACAG 952
Db
241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
QY
953 GCACAGGTGGGCGAGGCTTACGTGGGGGGCGCTCTCTGCACCTGATGACCTCCACTGC 1012
Db
261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
QY
1013 CCACCTAGTGCCTCCCAACCATCACAGCAGGAGGCTCCCAATGTGGCTCACGAGTGA 1072
Db
281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlnGluLeuLeuGly 300
QY
1073 GGGGGCTGCATGGCTTCTCCCAAAATTCATGCACCTGGCAGAGGAATTTGCTGGGA 1132
Db
301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
QY
1133 GGATGGCCAGAGACCCCAAGGAGGCTGCTGAGGGCAGAGGCCCTGCAGAGCACTTC 1192
Db
321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
QY
1193 TTGCTGATGATGCTCCCGCGAGCTGTACAGCAATTCGGGGTGACTATCAGACATGAC 1252
Db
341 IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
QY
1253 ATTGGCTGGAGTGAGGAGGCGCCAGCAGTCTCAAGCTCAGTGTGCTGCCGCTTTGTG 1312
Db
361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
QY
1313 CAGCTGCCCGAGGAGGCCCTGCTGAGAGCTTCCAGCAGATCCATGCTCTCTCTCCTCC 1372
Db
381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
QY
1373 ACCACCTGGATGACATCCTGCATGCTTCTCTGAAGTCACTGCTGCCCTGTGGTGGGA 1432
Db
401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
QY
1433 GGCTATCTGCTCATGCTGGCTTATGCTGTGACCATGCTGCGGTGGGACTGCGCCGAG 1492
Db
421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
QY
1493 TCCCAGGGTTCCTGGGGCCCTTCCCGGGTACTGCTGTGGCTTCCCGGTGGCTCAGGC 1552
Db
441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
QY
1553 CTGGGCTCTGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1612
Db
461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
QY
1613 TTTTGGCTCTGGGAATCGGCGTGGATGACGATTTCTTCTGCTGGCGCATGCTTCCACAG 1672
Db
481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
QY
1673 GCTCTGCTGGCACTTCCAGGAGCGCATGGCGAGTGTCTGTCAGCGCAGCGGCACC 1732
Db
501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
QY
1733 AGTGTGCTACTCACATCCATCAACAACTGCGCGCTTCCCTATGGCTGCTCTGCTTCC 1792
Db
521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
QY

Db 1793 ATCCCTGCGCTCGAGCCCTTCCCTACAGCGGCCATAGTGGTGGCTGCACCTTTGTA 1852
 QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
 Db 1853 GCCGTGATGCTTGCTTCCAGCCATCTCAGCTGGACCTACGGCGGCCACTGCCAG 1912
 QY 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
 Db 1913 CGCCTTGATGCTCTGCTGCTCTCCAGTCCCTCTCTGCTCAGTGATTCAGATCCTG 1972
 QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
 Db 1973 CCCAGAGAGCTGGGGAGCGGACAGTACAGTGGGCATTTGCCCACTCACTGCCACAGTT 2032
 QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
 Db 2033 CAAGCCCTTATCCCACTGTGAAGCCAGCAGCAGCATGTGTCACCATCTGCCCTCCCAA 2092
 QY 621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
 Db 2093 GCCCACCCTGGTGGCCCACTCTCAGCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
 QY 641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
 Db 2153 TCACACGGGACCTTTAGGGCCAGGAGGAGAGCAAGGAGGAGGAGGAGGAGGAGGAGTCC 2212
 QY 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTrpGlnPheAlaProLeuLeu 680
 Db 2213 CTGCCCTGTGCCGTGGATCTTGCCCATTTGCCCGCTATCATAGTTTGGCCCGTGTCTG 2272
 QY 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
 Db 2273 CTCAGTCATCATGCCAAGGCATCTGCTGCTCTTTGGTCTCTTCTGGGCTTGAGC 2332
 QY 701 LeuTrpGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
 Db 2333 CTCTACGGAGACCACTTTGGTGGCAAGACGGCTGGCCCTGACGGAATGTGTGCTCGGGC 2392
 QY 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTrpPheSerLeuTrpGluValAla 740
 Db 2393 ACCAAGGAGCATGCTTCTGAGCGGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452
 QY 741 LeuValThrGlnGlyGlyPheAspTrpAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
 Db 2453 CTGGTGACCCAGGCTGGCTTGACTACGCCCATTTCCCAACGCCCTCTTTGATCTGCAC 2512
 QY 761 GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr 780
 Db 2513 CAGCGCTTCAGTTCCTCAAGCGGGTGTGCCCCCACCAGGCCACCCCGCAC 2572
 QY 781 TrpLeuHisTrpTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
 Db 2573 TGGCTGCATATTACCGCACTGGCTACAGGGAATCCAGGCTGCCCTTTACCAGGACTGG 2632
 QY 801 AlaSerGlyArgIleThrArgHisSerTrpArgAsnGlySerGluAspGlyAlaLeuAla 820
 Db 2633 GCTTCTGGGGCATCACCGCCACTCGTACCGCAATGGCTCTGAGATGGGGCCCTGGCC 2692
 QY 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnProLeuAspPheSerGlnLeuThr 840
 Db 2693 TACAAGCTGCTCATCCAGACTGGAGCGCCAGGAGCCTCTGGATTTCCAGCAGCTGACC 2752
 QY 841 ThrArgLysLeuValAspArgGlyLeuIleProProGluLeuPheTrpMetGlyLeu 860
 Db 2753 ACAAGGAAGCTGGTGACAGAGAGGAGCTGATTCACCCCGAGCTCTTACATGGGGCTG 2812
 QY 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTrpPro 880
 Db 2813 ACCGTGTGGGTGAGCAGTGAACCCCTGGGTCTGGCAGCCTCACAGGCCAATCTTACCCC 2872
 QY 881 ProProGluTrpLeuHisAspLysTrpAspThrThrGlyGluAsnLeuArgIlePro 900
 Db 2873 CCACCTCTGAATGGCTGCACGACAAATACGACACACAGCGGGGAGAACCTTCGCATCCG 2932

QY 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
 Db 2933 CCAGCTCAGCCCTTGGAGTTTGGCCAGTTCCCTTCTGCTCGGTGGCCCTCCAGAGACT 2992
 QY 921 AlaAspPheValGluAlaIleGlnGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
 Db 2993 GCAGACTTTTGGAGGCCATCGAGGGGCCCGGCGAGCATGCGAGAGGCCGCCAGGCT 3052
 QY 941 GlyValHisAlaTrpProSerGlySerProPheLeuPheTrpGluGlnTrpLeuGlyLeu 960
 Db 3053 GGGGTGCAGCCTACCCAGCGGCTCCCTCTCTCTCTGCGAACAGTATCTGGGCCCTG 3112
 QY 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
 Db 3113 CGGCGCTGCTCTCTGCTGGCGTCTGCATCTGCTGCTGCTGCTCTCTCTCTCTCTGCT 3172
 QY 981 LeuLeuLeuLeuAnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
 Db 3173 CTGCTGCTCTCTCAACCCCTGGACGGCTGGCTCATAGTGTGCTGGCGATGATGACA 3232
 QY 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
 Db 3233 GTGGAACCTCTTGGTATCATGGGTTTCTGGGCATCAAGCTGAGTGCATCCCCGTGGTG 3292
 QY 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
 Db 3293 ATCCTTGTGGCTCTGTAGGCATTGGGTTGAGTTACAGTCCACGTCCAGTGGCTCTGGGCTTC 3352
 QY 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
 Db 3353 CTACACCCAGGAGCGCGAACCTTGGCGGCCCATGCCCTTGAGCACACATTGGCC 3412
 QY 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
 Db 3413 CCGGTGACCATGGGCGCATCTCCACATTGCTGGGTCTGCTCATGCTTGTGTGCTTCCAC 3472
 QY 1081 PheAspPheIleValArgTrpPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
 Db 3473 TTTGACTTCATTGTAAGGTACTTCTTTGGCGGCTGACAGTGTCTACGCTCTCTGGGCTC 3532
 QY 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
 Db 3533 CTCCTAGGACTCGTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 3592
 QY 1121 IleGlnMetTrpLysGluSerProGluIleLeuSerProProAlaProGlnGlyGly 1140
 Db 3593 ATACAGATGACAGGAAGCCAGAGATCTCTGAGTCCACCGAGTCCACAGGAGCGGG 3652
 QY 1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
 Db 3653 CTTAGTGGGGGATCT 3712
 QY 1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
 Db 3713 ACCGTGGGCATCCACCCACCCCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 3772
 QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
 Db 3773 CCCCCTTGGTCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCGAGTCCA 3832
 QY 1201 AlaThrGly 1203
 Db 3833 GCCACTGGG 3841

RESULT 2

AAD31576

ID AAD31576 standard; cDNA; 4030 BP.

XX

AC AAD31576;

XX

DT 18-JUN-2002 (first entry)

XX

DE	Human patched-2 (Ptc-2) cDNA.	
XX	Human; patched-2; Ptc-2; cell proliferation; differentiation; therapy;	
XX	cytostatic; testicular cancer; hedgehog protein signalling; ss.	
XX	Homo sapiens.	
XX	Key Location/Qualifiers	
XX	233..3844	
XX	CDS	
XX	/*tag= a	
XX	/product= "Human Ptc-2 protein"	
XX	US6348575-B1.	
XX	19-FEB-2002.	
XX	15-APR-1999; 99US-00293505.	
XX	15-APR-1998; 98US-0081884P.	
XX	(GETH) GENENTECH INC.	
XX	De Sauvage F, Carpenter DA;	
XX	WPI; 2002-215260/27.	
XX	P-PSDB; AAE19829.	
XX	Native human patched-2 polypeptide for treating disorders caused by	
XX	Hedgehog protein signaling such as testicular cancer, and for screening	
XX	cDNA libraries.	
XX	Example 1; Fig 1; 82pp; English.	
XX	The invention relates to an isolated sequence comprising a native human	
XX	patched-2 (Ptc-2) polypeptide. The invention also relates to signalling	
XX	and mediator molecules in the hedgehog (hh) cascade which are involved in	
XX	cell proliferation and differentiation. The isolated sequence is useful	
XX	for the treatment of disorders which are linked to Hedgehog, especially	
XX	Desert hedgehog expression, such as testicular cancer. It may also be	
XX	used as a hybridisation probe in a cDNA library to isolate Ptc-2 or its	
XX	homologues, and to diagnose whether a disorder is driven by Ptc-2 or	
XX	Hedgehog protein signalling. The present sequence is human patched-2	
XX	(Ptc-2) cDNA	
XX	Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;	
XX	Alignment Scores:	
XX	Pred. No.: 0 Length: 4030	
XX	Score: 6272.00 Matches: 1203	
XX	Percent Similarity: 100.00% Conservative: 0	
XX	Best Local Similarity: 100.00% Mismatches: 0	
XX	Query Match: 100.00% Indels: 0	
XX	DE: 6 Gaps: 0	
XX	US-09-990-046-2 (1-1203) x AAD31576 (1-4030)	
QY	1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20	
DB	233 ATGACTCGATCGCCGCCCTCAGAGAGCTGCCCGAGTTACACACCCCGAGCTCGAAC 292	
QY	21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40	
DB	293 GCAGCACCCAGAGCTTCTCTCTCGGATGCGGATCCAGAGACATTGTGGCAAGTCTTTC 352	
QY	41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60	
DB	353 CAGGGCCCTGCTTCTCTCTCGGATGCGGATCCAGAGACATTGTGGCAAGTCTTTC 412	
QY	61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleGluThr 80	
DB	413 CTGGAGCTGTGGCTTTGGGGCCCTGGCAATTAGTCTCCGCATGGCCATTATTAGACA 472	
QY	81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100	

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QY	1	MetThrArgSerProLeuArgGluLeuProProSerTyrThrProProAlaArgThr	20
Db	233	ATGACTCGATCGCGCCCTCAGAGCTGCCCGAGTTACACACCCAGCTCGAAC	292
QY	21	AlaAlaProGlnIleLeuAlaGlySerLeuIysAlaProLeuTrpLeuArgAlaTyrPhe	40
Db	293	GCAGACCCAGATCTTAGCTGGAGGCTGAGGCTCCACTCTGGCTTGTGCTACTTC	352
QY	41	GinglyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyIysValLeuPhe	60
Db	353	CAGGCGCTGCTCTTCTCTCGGATCGGGATCCAGAGACATTTGTGCAAGGCTCTTT	412
QY	61	LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr	80
Db	413	CTGGACCTGTTGGCCCTTTGGGCCCTGGCAATTAGTCTCCGATGGCCATTATGAGACA	472

Db 1553 CTTGGGCTCTGTGGCCCTGTGGCATCACCTTCAATGCTGGCCATACCCAGGTGTGCCT 1612
Qy 461 PheLeuAlaLeuGlyVileGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1613 TTTCTGGCTCTGGGAATCGGGTGGATGACGATTTCTCTGTGGCCATGCTTTCACAGAG 1672
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1673 GCTCTGCTGCACCCCTCTCCAGAGCGCATGGCGAGTGTCTGCAGCGCACGGGCACC 1732
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1733 AGTGTGTACTCATCATCATCAACAACATGGCCGCTTCTCTCATGGCTGCTCTGTTCC 1792
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1793 ATCCCTGCTGCTGCAGGCTTCTCCCTACAGCGGCATAGTGGTGGCTGCACCTTTGTA 1852
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
Db 1853 GCCGTGATGTGTCTTCCAGCCATCTCAGCCTGGACCTACGGCGGCCCATCTGCCAG 1912
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1913 CGCTTGTATGTCTCTCTCTCTCCAGTCCCTGCTCTCTCAGGTGATTCAGATCCTG 1972
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1973 CCCAGAGCTGGGGACGGGACAGTACAGTGGGCATGCCACCTCACTGGCCACAGTT 2032
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2033 CAAGCCCTTACCACACTGTGAAGCCAGCAGCCAGCATGTGTCTACCATCTCGCTCCCAA 2092
Qy 621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2093 GCCCACTGTGTGCCCCACCTCTGACCCACTGGGCTCTGAGCTTTCAGCCCTGGAGG 2152
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnIlyAlaAlaCysLysSer 660
Db 2153 TCCACAGGGACCTTCTAGCCAGGAGGAGGAGACAGGACAGGACGACCTGCAAGTCC 2212
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2213 CTGCCCTGTGCGCGCTGGAATCTTGCCATTTGCCCGCTATCAGTTTGCCCGTGTCTG 2272
Qy 681 LeuGlnSerHisAlaIlyAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2273 CTCAGTCAATGCAAGGCCATCGTGTGTGTCTTTTGGTGTCTTCTGGGCGCTGAGC 2332
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValProArgGly 720
Db 2333 CTCACGGAGCCACTTGTGTGCAAGCGCCCTGGGCCCTGACGGATGTGTGCTCTGGGCG 2392
Qy 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2393 ACCAAGAGCATGCTTCTGAGCGCCCGAGCTCAGGTACTTCTCCCTGTACAGGTGGCC 2452
Qy 741 LeuValThrGlnGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2453 CTGGTACCCAGGGTGGTCTTGACTACGCCCATTCGCCAACGCGCCCTCTTTGATCTGCAC 2512
Qy 761 GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr 780
Db 2513 CAGCGCTTCAGTTCCTCAAGCGGTGTGTGCCCCCAGCCGCGCACCCAGCCCGCCAGC 2572
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2573 TGGTGTCACTATTACCGCACTGGCTACAGGGAATCCAGGCTGCTTTGACACAGACTGG 2632
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2633 GCCTTCTGGGCGCATCACCCGCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692

Qy 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2693 TACAAGCTGTCTCATCCAGACTGGAGCCGCCAGAGCCCTCTGGATTTTCAGCCAGCTGACC 2752
Qy 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2753 ACAAGGAAGCTGGTGGACAGAGAGGACTGATTCACCCGAGCTCTTCTACATGGGGCTG 2812
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2813 ACCGTGTGGTGGACAGTACCCCTCTGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC 2872
Qy 881 ProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2873 CCACCTCTGAATGGCTGCACGAAATACGACACACAGGGGGAGAACCTTCGCATCCCG 2932
Qy 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
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Qy 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
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Qy 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db 3053 GGGGTGCAGCCCTACCCAGCGGCTCCCTTCTCTTGGGAACAGTATCTGGGGCTG 3112
Qy 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 3113 CGCGCTGTCTCTGTGTGGCGCTCTGCATCTCTGTGTGGTGGCTTCTCTCGTCTGTCT 3172
Qy 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db 3173 CTGCTGCTCTCAACCCCTGGAGCGGCTGGCCTCATAGTCTGTCTCGCGATGATGACA 3232
Qy 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db 3233 GTGGAACCTTTTGGTATCATGGGTTCTTGGGCATCAAGCTGAGTGCCATCCCGTGGTG 3292
Qy 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db 3293 ATCCCTTGTGGCTCTGTAGGCATTTGGCGTTAGTTACAGTCCACGTGGCTCTGGGCTTC 3352
Qy 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3353 CTGACACCCAGGGCAGCGGAACTGCGGGCGGCCCATGCGCTTTCAGCACATTTGGC 3412
Qy 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db 3413 CCCGTGACCGATGGGGCCATCTCCACATTTGTGGGTCTGTCTCATGCTTGTGGTTCGCCAC 3472
Qy 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db 3473 TTTGACTTCAITGTAAAGTACTTCTTTGCGCGCTGCAGTGTCTCACGCTCTGGGCTC 3532
Qy 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
Db 3533 CTCCATGAGCTGTGTGTCTGCTGCTGTCTGTCTCATCTCTGGGCGGCCCGCCAGAGTG 3592
Qy 1121 IleGlnMetTyrLysGlySerProGluIleLeuSerProProAlaProGlnGlyGly 1140
Db 3593 ATACAGATGTACAAAGGAAGCCAGAGATCTGTAGTCCACAGCTCCAGAGGAGGGGG 3652
Qy 1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db 3653 CTTAGTGGGGGGCATCTCTCTCCCTGCCCGCAGAGCTTTGCCAGAGTACTACCTCCATG 3712
Qy 1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db 3713 ACCGTGGCCATCACCCACCCCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3772

Sun Nov 28 09:38:31 2004

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QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
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Db 3773 CCCCCTGGCTCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACAGGTCCA 3832

QY 1201 AlaThrGly 1203
    |||||||
Db 3833 GCCACTGGG 3841

RESULT 3
ID ABX15919 standard; DNA; 4030 BP.
XX
AC ABX15919;
XX
DT 02-APR-2003 (first entry)
XX
DE Human cDNA for patched-2 with vector sequences.
XX
KW Human; patched-2; Dhh signalling; proliferation; differentiation; ds;
KW chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
KW basal cell carcinoma; neurodegenerative disorder; memory deficit;
KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
KW bone disease; skin disease; testicular disease; ulcer; lung disease;
KW pancreatic disease; diabetes; osteoporosis; SNP;
KW single nucleotide polymorphism; desert hedgehog.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..212
FT /tag= a
FT /note= "Vector sequence"
FT CDS 233..3844
FT /tag= b
FT /product= "Patched-2"
FT /replace= (3925,T)
FT /tag= c
FT /standard name= "Single nucleotide polymorphism"
FT misc_feature 3997..4030
FT /tag= d
FT /note= "Vector sequence"
XX
XX US2002156245-A1.
XX
XX 24-OCT-2002.
XX
XX 20-NOV-2001; 2001US-00990046.
XX
XX 15-APR-1998; 98US-0081884P.
XX 15-APR-1999; 99US-00293505.
XX (GETH ) GENENTECH INC.
XX
XX De Sauvage FJ, Carpenter DA;
XX WPI; 2003-182650/18.
XX P-PSDB; ABG74104.
XX
XX New nucleic acid, useful for manufacturing a medicament for diagnosing or
XX treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
XX e.g., testicular cancer.
XX
XX Example 1; Fig 1; 85pp; English.
XX
XX The invention relates to a new isolated nucleic acid encoding a
XX polypeptide having patched-2 biological activity, comprises DNA having at
XX least 95% sequence identity with a DNA molecule or its complement
XX encoding: (a) a human patched-2 polypeptide comprising the sequence
XX ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ARCC
XX Deposit No. 209778 designation). Also included are a vector comprising
XX the nucleic acid, a host cell transformed with the vector, a process for

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CC producing patched-2 polypeptides, an isolated native sequence of human
CC patched-2 polypeptide, a chimeric molecule comprising the vertebrate
CC patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
CC patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
CC hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
CC patched-2 that stimulates or enhances the normal functioning of patched-2
CC in the Dhh signalling pathway, screening for ant/agonists of patched-2
CC and diagnosing to determine whether a particular disorder is modulated
CC The nucleic acid is useful for manufacturing a medicament for diagnosing
CC or treating a disorder that is modulated by Dhh signalling e.g. tumour,
CC basal cell carcinoma, neurodegenerative disorders, memory deficit,
CC Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
CC Huntington's disease, schizophrenia, stroke, drug addiction, gut
CC diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
CC diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
CC Patched-2 may also be used to develop male contraceptives. The gene for
CC Patched-2 is located on human chromosome 1p33-34. The present sequence is
CC the human cDNA for patched-2 (along with some vector derived sequences)
XX
XX Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;
SQ
Alignment Scores: Length: 4030
Pred. No.: 0 Matches: 1203
Score: 6272.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 8
US-09-990-046-2 (1-1203) x ABX15919 (1-4030)
QY 1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
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Db 233 ATGACTCGATCGCGCCCTCAGAGAGTGCCTCCGAGATTACACACCCAGCTCGAACC 292

QY 21 AlaAlaProGlnLeuAlaGlySerLeuLeuAlaProLeuTrpLeuArgAlaTyrPhe 40
    |||||||
Db 293 GCAGACCCAGATCCTAGTGGAGCCTCAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352

QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
    |||||||
Db 353 CAGGGCTGTCTTCTCTCTGGGATGCGGATCCAGAGACATTGTGCAAGTCTCTTT 412

QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleGluThr 80
    |||||||
Db 413 CTGGGACTGTGGCTTTGGGGCCCTGGCATTTAGTCTCCGATGGCCATTATTAGACA 472

QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
    |||||||
Db 473 AACTTGGAAACAGCTCTGGGTAGAGTGGCGAGCGGGTGAGCCAGGAGCTGATTACACC 532

QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
    |||||||
Db 533 AAGGAGAGCTGGGGGAGGAGGCTGCATACACTCTCAGATGCTGATACAGACCCGACGC 592

QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGluAlaLeu 140
    |||||||
Db 593 CAGGAGGGAGAGAAACATCTCACACCCGAGCACTTGGCCCTCCACCTCAGGAGCCCTC 652

QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
    |||||||
Db 653 ACTGCAGTAAAGTCAAGTATCATCTTATGGGAGTCTGGGATTTGAAACAAATCTGC 712

QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
    |||||||
Db 713 TACAAGTCAGGAGTTCCTTATTGAAATGGAATGATTGATGGATGATTGAGAAGCTG 772

QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
    |||||||
Db 773 TTTCCGTGCGTGATCTCTCACCCCTCGACTGCTTTCTGGGAGGAGGCCAAATCTCAAGG 832

QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTyrThrAsnLeuAspProGluGln 220
    |||||||

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Db 833 GGCTCCGCTACTCTCCCGCGCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892
QY 221 LeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 893 CTGCTGGAGGAGCTGGGTCCCTTTGGCTTCCCTTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952
QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 953 GCACAGGTGGGCCAGGCTACGTGGGGCGGCCCTGTCTGCACCTGTATGACCTCCACTGC 1012
QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 1013 CCACCTAGTGGCCCAACCAATCACAGCAGGAGGCTCCCAATGTGGCTCAAGAGCTGAGT 1072
QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
Db 1073 GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCACTGGCAGGAGGAATTCCTCTGGGA 1132
QY 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 1133 GGCAATGGCCAGACACCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192
QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 1193 TTGCTGATGATGTCCTCCCGCCAGCTGTACAGCATTTCCGGGGTGACTATCACACACATGAC 1252
QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal 360
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QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
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QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db 1373 ACCACCTGTGATGACATCCCTGCAATGGCTTCTGAAATCAGTCTGCGCGGTGGTGGGA 1432
QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1433 GGCTATCTGCTCATGTGGCCCTATGCTGTGTGACCATGCTGGGTGGGACTGCGGCCAG 1492
QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1493 TCCCAAGGTTCCGTGGCCCTTGGCGGGTACTGCTGTGGCCCTGGCGGTGGCTCAGGC 1552
QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1553 CTGGGCTCTGTGCCCTGCTCGGCATACACCTTCAATGTGCCACTACCCAGGTGCTGCCT 1612
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Db 1793 ATCCCTGGCTGCGAGCCTTCTCCCTACAGGGCCCATAGTGTGGTGGCTGCACCTTTGTA 1852
QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuAlaArgHisCysGln 560
Db 1853 GCCGTGATGCTGTCTTCCAGCCATCTCCAGCTGGACCTACGGCGGGCCACTGGCCAG 1912
QY 561 ArgLeuAspValLeuCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1913 GGCCTTGTATGTGCTGTGCTGTCTTCCAGTCCCTGCTCTGCTCAGGTGATTTCAGATCTGT 1972

QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1973 CCCCAGGAGCTGGGGACGGGACAGTACAGTGGGCATTTGCCACTCTACCTGCCACAGTT 2032
QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCAGCATGTGGTCACCATCTGCTCCCTCCCAA 2092
QY 621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2093 GCCCACCCTGGTGGCCCCCACCCTTTCGACCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
QY 641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 2153 TCCACACGGGACCTTCTAGCCAGGAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGTCC 2212
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Db 2273 CTCCAGTCATGCCAAGGCCATCGTCTGGTCTCTTTGGTCTCTTCTGGGCTCGAGC 2332
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Db 2333 CTCTACGGAGCCACCTTGGTGCAGAGCGCTGGCCCTGACGATGTGGTGGCTCGGGGC 2392
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Db 2933 CCAGCTCAGCCCTTGGAGTTTGGCCAGTTTCCCTTCTGCTGCTGGCTCCAGAGACT 2992
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QY 941 GlyValHisAlaTyrProSerClySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
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 DB 3113 CGGCGCTGCTTCTGCTGCGGCTGTGCATCTGCTGCTGGTGACITTCCTGCTGTGCT 3172
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 DB 3473 TTTGACTTCTATTGTAGGTACTTCTTGGCGGCTGACAGTGTCTCGCTCTCTGGGCTC 3532
 QY 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
 DB 3533 CTCATGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3592
 QY 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly 1140
 DB 3593 ATACAGATGTACAGGAAGAACCCAGAGATCTGAGTCCACAGCTCCACAGGAGGCGGG 3652
 QY 1141 LeuArgTyrGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
 DB 3653 CTTAGTGGGGGCGATCTCTCTCCCTGCCCGACAGCTTGGCAGAGTACTACCTCCATG 3712
 QY 1161 ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
 DB 3713 ACCGTGGCCATCCACCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3772
 QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
 DB 3773 CCCCCTTGGTCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAAGTCCA 3832
 QY 1201 AlaThrGly 1203
 DB 3833 GCCACTGGG 3841
 RESULT 4
 ID AAX89478 standard; cDNA; 4391 BP.
 AC AAX89478;
 XX AAX89478;
 DT 03-DEC-1999 (first entry)
 XX Human ptc-2 cDNA.
 DE Patched-2; ptc-2; human; hedgehog receptor; neurotropic; neuroprotective;
 KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
 KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
 KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
 KW graft; transplant; treatment; nervous system injury; chemical injury;
 KW val injury; infection; inflammatory; tumor-induced injury; ageing;
 KW Alzheimer's disease; chronic neurodegenerative disease; innervation;

Parkinson's disease; Huntingdon's chorea; amyotrophic lateral sclerosis;
 spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
 peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
 atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
 lesion-induced death; neuron regeneration; damage repair; skeletal;
 cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
 prosthetic cartilage device; spermatogenesis; fertility enhancer; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 CDS 297..3908
 /tag= a
 /product= "ptc-2"

XX WO929854-A1.

XX 17-JUN-1999.

XX 08-DEC-1998; 98WO-US026009.

XX 08-DEC-1997; 97US-0067940P.

XX (ONTO-) ONTOGENY INC.

XX Bumcrot DA;

XX WPI: 1999-561298/47.

XX P-PSDB; AAY28444.

XX New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
 PT prevention and/or reduction of the severity of neurological conditions.

XX Claim 2; Page 66-72; 80pp; English.

XX This invention describes a novel recombinantly produced human patched-2
 CC (ptc-2) polypeptide which has neurotropic, neuroprotective, cardiant,
 CC antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
 CC protein is a hedgehog receptor and is therefore capable of modulating
 CC hedgehog signalling, and so affect a number of hedgehog-mediated
 CC biological activities. The human patched-2 (ptc-2) protein can be used to
 CC screen for modulators, antagonists and agonists, which are likely to play
 CC an important role in the modulation of cellular proliferation and
 CC maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
 CC tissues during disease states. Modulators of ptc-2 protein can be used
 CC for in vivo reformation of tissue; to improve grafting and morphology of
 CC transplanted tissue; for the treatment, prevention and/or reduction of
 CC the severity of neurological conditions deriving from: injury to the
 CC nervous system including traumatic injury, chemical injury, vascular injury
 CC and deficits (such as ischemia resulting from stroke), together with
 CC infectious/inflammatory and tumor-induced injury; ageing of the nervous
 CC system including Alzheimer's disease; chronic neurodegenerative diseases
 CC of the nervous system including Parkinson's disease, Huntington's chorea,
 CC amyotrophic lateral sclerosis, as well as spinocerebellar degenerations;
 CC and chronic immunological diseases of the nervous system including
 CC multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
 CC of autonomic disorders of the peripheral nervous system, and endocrine
 CC disorders affecting the innervation of smooth muscle and endocrine
 CC tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
 CC Antagonists of ptc-2 protein can be used to prevent differentiation of
 CC cells in culture, as well as for treatment of chronic pain syndromes.
 CC Agonists may be used to rescue neurons from lesion-induced death as well
 CC as neuron regeneration, in diseases such as CNS trauma infarction, (viral)
 CC infection, metabolic disease, nutritional deficiency, toxic agents, and
 CC so on. ptc-2 therapeutics may also be used for the repair of central and
 CC peripheral nerve damage, for repair and regeneration of non-neuronal
 CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
 CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
 CC for generation of prosthetic cartilage devices, and to induce
 CC spermatogenesis and as fertility enhancers. This sequence encodes the
 CC human ptc-2 protein described in the invention

XX Sequence 4391 BP; 769 A; 1475 C; 1224 G; 923 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 0 Length: 4391
 Score: 6248.00 Matches: 1200
 Percent Similarity: 99.75% Conservative: 0
 Best Local Similarity: 99.75% Mismatches: 3
 Query Match: 99.62% Indels: 0
 DB: 2 Gaps: 0

US-09-990-046-2 (1-1203) x AAX89478 (1-4391)

QY 1 MetThrArgSerProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
 DB 297 ATGACTCGATCCGCCCTCAGAGAGCTGCCCGGAGTTACACACCCCGAGTCAACC 356
 QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
 DB 357 GCAGCACCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTGGTCTTACTTC 416
 QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 DB 417 CAGGCGCTGCTCTCTCTCGGATGCGGATCCAGAGACATTTGGCAAGTGTCTTT 476
 QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
 DB 477 CTGGGACTGTTGGCTTTGGGCGCCCTGGCATTAGGTCTCCGATGGCCATTATTGAGACA 536
 QY 81 AsnLeuGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
 DB 537 AACTTGAACAGCTCTGGTAGAGTGGGAGCGGAGCTTGGGAGGAGCTGCATTTACACC 596
 QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 DB 597 AAGGAGAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGCCGACGC 656
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
 DB 657 CAGAGGAGAGAGAACATCTCCACACCGCAAGCACTTGGCCCTCCACCTCCAGGAGCCCTC 716
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 DB 717 ACTGCCAGTAAGTCCCAAGTATCACTCTATGGGAAGTCTTGGGATTTGAACAAATCTGC 776
 QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
 DB 777 TACAAGTCAGGAGTTCCTCTATTGAAATGGAATGATTCAGCGGATGATTGAGAGCTG 836
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
 DB 837 TTTCCGTGGTATCTCACCCCTTCGACTGTCTTGGGAGGAGCCAACTCCAAAGG 896
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
 DB 897 GGCCTCGCTACTGTCGCGCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 956
 QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 DB 957 CTGCTGGAGGAGCTGGGTCCCTTTGCTCCCTTGGGGCTTCGGGAGCTGTAGACAG 1016
 QY 241 AlaGlnValGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
 DB 1017 GCACAGTGGGCGAGCCCTACGTGGGCGGCGCCCTGTCTGACCCCTGATGACCTCCACTGC 1076
 QY 261 ProProSerAlaProAsnHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
 DB 1077 CCACCTAGTGGCCCCCAACCATCACAGCAGGAGGCTCCCAATGTGGCTCAGAGTGA 1136
 QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuGly 300
 DB 1137 GGGGCTGCCATGGCTTCTCCACAAATTCATGCATGGCAGGAGGAATGCTGTCTGGGA 1196
 QY 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320

DB 1197 GGCATGGCCAGAGACCCCAAGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1256
 QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
 DB 1257 TTGCTGATGAGTCCCGCCAGCTGACAGACATTTCCGGGGTGACTATCAGACACATGAC 1316
 QY 341 IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
 DB 1317 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGTCTAAGCCTGGCAGCGGCTTTGTG 1376
 QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
 DB 1377 CAGCTGGCCCGAGAGGCCCTGCTCGAGAACGCTTCCAGCAGATCATGCTCTCTCTCC 1436
 QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
 DB 1437 ACCACCTGGATGACATCTCGATCGCTTCTTGAAGTCAGTGTGCGCGCTGTGTGGTGA 1496
 QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTyrAspCysAlaGln 420
 DB 1497 GGCTATCTGCTCATGCTGGCTATGCTGTGTGACCATGCTGGGTGGGACTGCGCCAG 1556
 QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
 DB 1557 TCCAGGGTTCCTGGGGCTTGGCGGGTACTGCTGGTGGCGCTGGCGCTGCGCTCAGGC 1616
 QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrGlnValLeuPro 460
 DB 1617 CTTGGCTCTGTGCCCTGCTGGCATCACCTTCAATGCTGCACCTACCCAGGTGTGCTCC 1676
 QY 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
 DB 1677 TTCTTGGCTCTGGGAATCGCGTGGATGACGTATTCCTGCTGGCGCATGCTTCCAGAG 1736
 QY 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
 DB 1737 GCTTGTGCTGGCAGCCCTCTCCAGGAGCGATGGCGAGTGTCTGCGCGCACCTTCCAGAG 1796
 QY 501 SerValValLeuThrSerIleAsnAspMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
 DB 1797 AGTGTGCTACTCATCTCCATCAACATGCGCGCTTCTCATGGCTGCGCTCTGCTCC 1856
 QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
 DB 1857 ATCCCTGCGTGGAGCTTCTCCCTACAGCGCGCATAGTGTGGCTGCACCTTTGTA 1916
 QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
 DB 1917 GCGTGTATGCTTGTCTTCCAGCCATCTTTCAGCTTGGACTTACGGCGGCGCACTGCCAG 1976
 QY 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
 DB 1977 CGCCTTGATGTCTGTGCTGCTTCCAGTCCCTGCTGTGCTCAGGTGATTGAGATCCTG 2036
 QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
 DB 2037 CCCCAGGAGCTGGGGAGCGGAGCAGTACAGTGGGCATTGCCCATCTCACTGCCACAGTT 2096
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 DB 2097 CAGCCTTTTACCATGTGGAGCCAGCAGCAGCATGTGTGTGCTCAGGTGATTCAGATCCTG 2156
 QY 621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
 DB 2157 GCCCAGCTGTGGCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCCAGCCTGGAGG 2216
 QY 641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
 DB 2217 TCCACAGGGACCTTCTAGGCCAGGAGGAGACAGGACAGGAGGAGGCTGCAAGTCC 2276
 QY 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
 DB 2277 CTGCCCTGTGCCGCTGGAATCTTGCCCAATTTGCCCGCTATCAGTTTGGCCCTGTGCTG 2336

Isolated human protein capable of participating in human patched gene/Sonic hedgehog pathway during embryonic development is used in medicament for treatment of condition involving tumors such as basal cell carcinoma.

Claim 4; Page 45; 55pp; English.

This cDNA is derived from the novel human patched 2 gene (PTCH2), which has been localised by radiation hybrid mapping to chromosome 1p32-35 with D1S211 and W11404 as closest flanking markers and with an estimated localisation 5.5 cR from D1S443. This region is often lost by LOH in various different tumour types, such as neuroblastoma, melanoma and breast and colon cancer. PTCH2 is a candidate for a tumour suppressor gene in this region. It is also a candidate gene for involvement in familial melanoma CMM1, modifier locus for familial adenomatous polyposis hMOM1 and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene exist (see AAA09082-84). PTCH2 is capable of participating in the PTCH2 gene patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic development and/or carcinogenesis. The isolated human protein is useful as a medicament for the treatment of a condition involving tumours such as BCC (basal cell carcinoma). The nucleic acid is useful in gene therapy, and for use as a probe, primer or a diagnostic agent

Sequence 3453 BP; 600 A; 1135 C; 989 G; 729 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3453
Score: 5911.00 Matches: 1139
Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 3
Query Match: 94.24% Indels: 0
DB: 3 Gaps: 0

US-09-990-046-2 (1-1203) x AAA09081 (1-3453)

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PT	Db	613	GGCTCCGCTACCTTGGCCGGCCGGGATATCCAGTGGACCAACCTGGATCCAGAGCAG	672
XX	Qy	221	LeuLeuGluLeuLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240
CC	Db	673	CTGCTGGAGGAGCTGGGTCCCTTTCCCTTCAGGAGCTTCGGGAGCTCTAGACAAG	732
CC	Qy	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys	260
CC	Db	733	GCACAGTGGGCCAGGCTACGTGGGGCGGCCCTGTCTGCACCTGTATGACTCCACTGC	792
CC	Qy	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280
CC	Db	793	CCACTAGTCCCCCAACCATCACAGGAGGAGCTCCCAATGTGGCTCAGAGCTGAGT	852
Qy	Qy	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly	300
Db	Db	853	GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCACCTGGCAGGAGGAATTGCTGGGA	912
Qy	Qy	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320
Db	Db	913	GGCATGCCAGAGACCCCAAGGAGAGCTCTGAGGCGAGAGCCCTGCAGAGACCTTC	972
Qy	Qy	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnTrpHisAsp	340
Db	Db	973	TTGCTGATGAGTCCCGCCAGCTGTAGAGCANTTCCGGGGTGACTATCAGACATGAC	1032
Qy	Qy	341	IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal	360
Db	Db	1033	ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGCTCTACAGCTGGCAGCGCGCTTTGTG	1092
Qy	Qy	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380
Db	Db	1093	CAGCTGGCCCGAGGAGCCCTGCTGAGAACGCTTCCAGCAGATCCATGCTCTCTCTCC	1152
Qy	Qy	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400
Db	Db	1153	ACCACCTCGATGACATCTGCTGATGCTTCTCTGAAAGTCAGTGCTGCCGTGGTGGGA	1212
Qy	Qy	401	GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln	420
Db	Db	1213	GGCTATCTCTCATGTGCTGCTATGCTGTGTGACCATCTGCGGTGGAGCTCGGCCAG	1272
Qy	Qy	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly	440
Db	Db	1273	TCCAGGGGTTCGTGGGCTTCCGGGGTACTGCTGTGGGCTTGGCGCTCAGGC	1332
Qy	Qy	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro	460
Db	Db	1333	CTTGGGCTCTGNGCCCTGCTCGGATACCTTCAATGTGCCACTACCCAGGTGTGCC	1392
Qy	Qy	461	PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu	480
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Qy	Qy	481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr	500
Db	Db	1453	GCTCTGCTGGCACCCCTCTCCAGGAGCGCATGGCGGAGTGTCTCAGCGCACCGGCACC	1512
Qy	Qy	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaLeuValPro	520
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Qy	Qy	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540
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Qy	Qy	541	AlaValMetLeuValProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560

Db	1633	GCCGTGATGCTTGTCTTCCAGCCATCTCAGCCTGCGACTACGGGGCGCCACTGCCAG	1692	QY	921	AlaAspPheValGluAlaIleGluGlyAlaAraGAlaAlaCysAlaGluAlaGlyGlnAla	940
QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580	Db	2773	CGAGACTTTTGTGAGGCCATCGAGGGGCCCCGGGAGCATGCGCAGAGCCCGCCAGGCT	2832
Db	1693	CGCCTTGATGTCTGCTGCTTCTCCAGTCCCTGCTGCTCAGGTGATTCAGATCCTG	1752	QY	941	GlyValHisAlaTyrProSerGlySerPropheLeuPheTyrPheGlnTyrLeuGlyLeu	960
QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600	Db	2833	GGGTTGACGCGCTACCCAGCGGCTCCCTCTTCTTGGGAAACAGTATCTGGGCGCTG	2892
Db	1753	CCCCAGAGCTGGGGACGGGACAGTACCAGTGGGCAITGGCCACCTCACTGCCACAGTT	1812	QY	961	ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla	980
QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620	Db	2893	CGGCGTGTCTTCTGCTGCGCCCTGCACTCTGCTGTGTCACATTTCTCTGCTGCTGCT	2952
Db	1813	CAAGCCTTTACCCACTGTGAGCCAGCAGCAGCATGTGGTCAACATCTCTGCTCCCAA	1872	QY	981	LeuLeuLeuLeuAsnProTyrThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr	1000
QY	621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640	Db	2953	CTGTGCTCTCTCAACCCCTGGACGCTGCCTCATAGTCTGCTGCTGCGATGATGACA	3012
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Db	1933	TCACACGGGACCTCTAGGCCAGGAGGAGACCAAGGAGGAGGAGGCTCAAGTCC	1992	QY	1021	IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe	1040
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QY	681	LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700	Db	3133	CTGACCCAGGAGCGGAACTTCGGGGCGCCCATGCTTGAGCACACATTTGCC	3192
Db	2053	CTCCAGTCAATCTAAGGCCATCGTGTGTGTCTTTGGTGTCTCTCTGCGCCTGAGC	2112	QY	1061	ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis	1080
QY	701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly	720	Db	3193	CCCGTGACCGATGGGGCCATCTCCATTTGCTGGTCTGTCTCATGCTGTGCTGTCCAC	3252
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QY	721	ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740	Db	3253	TTTGACTTCATTGTAAGTACTCTTTTGGCGCGCTGACAGTCTCAGCTCTCTGGGCTTC	3312
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QY	761	GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr	780	Db	3373	ATACAGATGTACAAGAAAGCCAGAGATCTCTGAGTCCACAGCTCCACAGGAGGCGG	3432
Db	2293	CAGCGCTTCAGTTCCCTCAAGGGGGTGTGCTGCCCCCAGCCCGCCAGGACCCCGCAC	2352	QY	1141	LeuArg	1142
QY	781	TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTyr	800	Db	3433	CTTAGG	3438
Db	2353	TGGCTGCATATTACCGCACTGGCTACAGGGATCCAGGCTGCTTTGACCAAGTGG	2412	RESULT 6			
QY	801	AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla	820	AAA09084			
Db	2413	GCTTCTGGCGCATCACCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC	2472	ID	AAA09084	standard; DNA; 12886 BP.	
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Db	2473	TACAACTGCTCATCCAGCTGGAGAGCCCGCAGAGCTTCGGAATTCAGCCAGCTGACC	2532	XX	10-AUG-2000	(first entry)	
QY	841	ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu	860	XX	Human	patched-like gene (PTCH2) genomic DNA.	
Db	2533	ACAAGGAAGCTGGTGGACAGAGAGGACTGATTCCACCGAGCTCTTCTACATGGGGCTG	2592	XX	Patched 2;	PTCH2; tumour suppressor; familial melanoma CMM1;	
QY	861	ThrValTrpValSerSerAspProLeuGlyLeuAlaSerGlnAlaAsnPheTyr-Pro	880	KW	familial	adenomatous polyposis; hMomi; Michelin tire Baby Syndrome;	
Db	2593	ACCGTGTGGTGGAGTGCCTGGCTGTGGCTGCGAGCCTCACAGGCCAATCTTACCCCC	2652	KW	sonic	hedgehog; SHH; development; carcinogenesis; cytosstatic;	
QY	881	ProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro	900	XX	basal	cell carcinoma; gene therapy; chromosome 1p32-35; ds.	
Db	2653	CCACTCTGTAATGGCTGCACACACAAATACACACCCAGGGGAGAACTTCGATCCCG	2712	OS	Homc	sapiens.	
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FT          WO2000020037-A1.
FT          13-APR-2000.
FT          06-OCT-1999; 99WO-SE001784.
FT          06-OCT-1998; 98SE-00003393.
FT          (KARO-) KAROLINSKA INNOVATIONS AB.
FT          (PHAA ) PHARMACIA & UPJOHN CO.
FT          Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
FT          Hollingsworth RE;
FT          WPI; 2000-303645/26.
FT          P-PSDB; AAY92225, AAY92703.
FT          Isolated human protein capable of participating in human patched
FT          gene/Sonic hedgehog pathway during embryonic development is used in
FT          medicament for treatment of condition involving tumors such as basal cell
FT          carcinoma.
FT          Claim 5; Page 46-49; 55pp; English.
FT          This genomic DNA comprises the novel human patched 2 gene (PTCH2), which
FT          has been localised by radiation hybrid mapping to chromosome 1p32-35 with
FT          DIS211 and W11404 as closest flanking markers and with an estimated
FT          localisation 5.5 cR from DIS443. A splice variant exists which is
FT          generated by 2 cRms of exon 21. This region is often lost by LOH in
FT          various different tumour types, such as neuroblastoma, melanoma and
FT          breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
FT          gene in this region. It is also a candidate gene for involvement in
FT          familial melanoma CMM1, modifier locus for familial adenomatous polyposis

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CC hMOM1 and Michelin Tire Baby Syndrome. Splice variants of the PTH2 gene
 CC exist (see AA09082-84). PTH2 is capable of participating in the human
 CC patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic
 CC development and/or carcinogenesis. The isolated human protein is useful
 CC as a medicament for the treatment of a condition involving tumours such
 CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
 CC therapy, and for use as a probe, primer or a diagnostic agent
 XX
 SQ Sequence 12886 BP; 2789 A; 3817 C; 3472 G; 2807 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 0 Length: 12886
 Score: 4692.50 Matches: 1166
 Percent Similarity: 38.40% Conservative: 1
 Best Local Similarity: 38.37% Mismatches: 13
 Query Match: 74.66% Indels: 1869
 DB: 3 Gaps: 20

US-09-990-046-2 (1-1203) x AA09084 (1-12886)

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DB	1107	CAGATCCTAGCTGGAGCCTGAAGCTCCACTCTGGCTTCGTCTTACTTCCAGGGCTG	1166
QY	44	LeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeu	63
DB	1167	CTCTCTCTCTGGGATCGGGATCCAGAGACATTTGTGCAAGTGTCTTCTTGGGACTG	1226
QY	64	LeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGlnThrAsnLeuGlu	83
DB	1227	TTGGCCCTTTGGGCCCCCTGGCATATTAGTCTCCGCATGGCCATTATTGAGACAACTTGGAA	1286
QY	84	GlnLeuTrpValGlu	88
DB	1287	CAGCTCTGGGTAGAAGTAAAGTTGTGGACACTGGCCATAGCTGCTCAGGTATGTGTAGCC	1346
QY	88	-----	88
DB	1347	CAGACAAGAACGGGTGAGGAGCTGGCTACTGAGCTCTAGCAGCCTGGCCCTGGGGCT	1406
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DB	1407	GGAGGGTCACTGTCTGGCCAGAGTCTTACACCTGGGCATCTAGGACACCGTTCCTCC	1466
QY	88	-----	88
DB	1467	ACACCATAAATGGACATCTGCAGATGTTAGACCTTGTGAATTTGGGTGTATAGAATAATT	1526
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DB	1527	GTCTGTGATTTTGTCTTAAGCCCTAGACCACACAGAAATCCGAGAGCCACACACCAG	1586
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QY	88	-----	88
DB	1707	TGGGAGGCCCTCAGAGTTAGAGCCCTTCCCAAGTCTTGACCCGCTAGGCCCTTTCC	1766
QY	89	-----ValGlySerArgValSerGlnGlnLeuHis	99
DB	1767	CCCCCAGCTTCTCTCTTGTCTCTGGCAGTGGGCGAGCGGTGAGCCAGAGTGCATTA	1826
QY	99	rThrLysGlnLysLeuGlyGlnGluAlaIaTyrThrSerGlnMetLeuIleGlnThrAl	119
DB	1827	CACCAAGAGAGAGCTGGGGGAGGAGCTGCATACACCTCTCAGATGCTGATACAGCCGC	1896
QY	119	aargGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAl	139

DB	1887	ACGCCAGGAGGAGAGAACATCTCACACCCGAAGCACTTGGCCTCCACCTCAGGAGC	1946
QY	139	aleuThrAlaSerLysValGlnValSerLeuTyrGlyLysSer	153
DB	1947	CCTCACTGCCAGTAAAGTCCAAAGTATCACTCTATGGGAAAGGT-GAGTCTGGGTGAGCCCC	2005
QY	153	-----	153
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QY	163	rGlyValProLeuIleGluAsnGlyMetIleGlu	174
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DB	2186	AGGCAGAACTTTTCTGTAGCTGGGAGGACTCAGAGACCGAGCAAGCCCAACAGCCCTGC	2245
QY	174	-----	174
DB	2246	AATCTGCCCTTTAAAACTAAGGAGGGGATTCAGAGGGGCATCTCTACAAGGTGTGGG	2305
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DB	2306	GCAGGACTGACGTGGCCCGGGGTATCTCTGGCAGATGATTGAGNAGCTGTTCCGTGGT	2365
QY	184	lIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTy	204
DB	2366	GATCTCACCCCTCTGACTGCTTCTGGGAGGAGCAAACTCCAGGGGGCTCCGGCTA	2425
QY	204	rLeuProGly	207
DB	2426	CCTGCCGTG-AGTSCCACTCTGGGGCCCTGCTTCATCTCCGCTGGGAGCTCTCCGAGC	2484
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Qy 207 ----- 207
Db 3025 CGCCCCCAGCAGATTTGGAGCCTGGGTTCGTCCTCGACCCCTCACCAACTATAGGCTT 3084
Qy 208 -----ArgProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuG1 223
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Db 3145 GGAGCTGGTCCCTTTGCTCCCTTGGGGCTTCGGGAGCTGCTAGACAAGGCACAGGT 3204
Qy 243 lGlyGlnAlaTyrrValGlyArgProCysLeuHisProAspAspLeuHisCysProProSe 263
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Db 4585 CCTATCCACCCCTGTTTCTC-CAGCTGGCCAGAGGCCCTGCTGAGAGCTTCCAGC 4643
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Db 4644 AGATCCATGCTTCTCTCCACACCCCTGATGACATCTGCAATGGTCTCTGAAAGTCA 4703
Qy 394 erAlaAlaArgValValGlyGlyTyrrLeuLeuMetLeu ----- 406
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Qy 406 ----- 406
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QY	487	-----	487	Db	6441	MAGGACATGCTTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTG	6500
Db	5363	ATACGTACATGTACCCAAATAAATGTAGCCACTGTGTATTANGACTGCCCCACCTCTGCAC	5422	QY	742	ValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGln	761
QY	487	-----	487	Db	6501	GTACCCAGGGTGGCTTTGACTACGCCCACTCCCAAGCGCCCTCTTTGATCTGTGACCCAG	6560
Db	5423	CCCAAGTTCTGAGCCTCCCTTCACTCCACTTTGACACGGCCCTCCCTTGTGACCTGA	5482	QY	762	ArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrp	781
QY	488	-----	488	Db	6561	CGCTTCAGTTCCCTCAGCGGTGTCTGCCCAACCGCCACCCAGGACACCCCGCACCTGG	6620
Db	5483	GGGAGCTCCCACTCTGTCTGGCAGAGCGCATGGCGAGTGTCTGCAGCGCACGGGC	5542	QY	782	LeuHisTyrTyrArgAsnTrpLeuGlnGlyIle	792
QY	500	ThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuVal	519	Db	6621	CTGCACCTATTACCGCAACTGGCTACAGGGTGA - GAGGCGAGGAGACGGGAGGAGGGGT	6679
Db	5543	ACCAGTGTCTACTCATCATCAACCATGCGCCCTTCTTCATGGCTGCCCTGTT	5602	QY	792	-----	792
QY	520	ProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPhe	539	Db	6680	GCTGAGGGAGAAACGCCCTGGGGCCACCAGCTAATAGAACCCCTATCTCGTCTCCCCCA	6739
Db	5603	CCCATCCCTGGCTGCGAGCTTCTCCCTACAGCGGCCCATAGTGTGGTGTGCACCTTT	5662	QY	793	-----	810
QY	540	ValAlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCys	559	Db	6740	GGAATCCAGCTGCTTTTGACAGGACTGGGCTTCTGGGGCATCACCCGCCACTCGAC -	6798
Db	5663	GTAGCGTGATGCTGTCTTCCAGCGCATCTCAGCCCTGGACCTACGGCGGCGCACTGC	5722	QY	811	ArgAsnGlySerGluAspGlyAlaLeuAlaTyrIleLeuIleGlnThrGlyAspAla	830
QY	560	GlnArgLeuAspValLeuCysCysPheSer	569	Db	6799	CGCAATGGCTCTGAGGATGGGGCCCTGGCTACAAGCTGTCTATCCAGACTGGAGAGGCC	6858
Db	5723	CAGCGCTTGTGTGCTCTGCTGTTCTC - CAGTACTGTGTGGCGGCCAGCCCTTCT	5781	QY	831	GlnGluProLeuAspPheSer	837
QY	569	-----	569	Db	6859	CAGGACTTCTGGANTTTCAGCCAGTTGGGAGGGCTGGAGGGTCCACTAGTACAGG	6918
Db	5782	CCCGTGACCCAGCGCTGCTCCCTCACCAGCATTTCAAGGCACAGACCTGTATCCA	5841	QY	838	-----	842
QY	570	-----	570	Db	6919	GCTGAGGCTCTTGGGCCCCAGGCTTACGCCCTCTCTGCTCTGCTGAGCTGACCAAGG	6978
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QY	605	HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal	624	Db	7039	TGGGTGAGCAGTACCCCTGGGTCTGGAGCTTCACAGGCAACTTACCCCCCACT	7098
Db	5962	CACGTGAGCCAGCAGCCACATGTGTCAACATCTCTGCTCCCAAGCCACCTGGT	6021	QY	883	ProGluTrpLeuHisAspLysTyrAspThrGlyGluAsnLeuArg	898
QY	625	ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644	Db	7099	CCTGAATGGCTGCACGACAATAACGACACCGGGGAGAACTTTCGAGTGTCTTGG	7158
Db	6022	CCCCACCTTCTGACCCACTGGGCTCTGAGTCTTTCAGCCCTGGAGGTTCCACAGGGAC	6081	QY	898	-----	898
QY	645	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664	Db	7159	GGGAGCTCGGCAAGAGCCTCAGCCTCGCCCCACACAAGCCCTGAGCCTGAGGCCCTGCC	7218
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QY	665	ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis	684	Db	7219	ACTCTGCCCGTGTCTACCGCCCTGTCCCTCTTCTCCCTTCCCTTCCCTCCCTCCAC	7278
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QY	685	AlaLysAla	687	Db	7279	AGTCCCGCAGCTCAGCCCTTGGAGTTTGGCCAGTTCCCTTCTCTGCTGCTGCTCCA	7338
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QY	687	-----	687				

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 QY 1119 ----- 1119
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 Db 9857 GCTTCCCAACAGTCATGGTAATCCCCAGCAGATGCTTAAGGGGACGGGACCCCGGG 9916
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 AAZ31728
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 XX AC AAZ31728;
 XX AC
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 DT 19-JAN-2000 (first entry)
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 XX Human patched-2 coding sequence partial clone 3A.
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 KW Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
 KW cell proliferation; cell differentiation; testicular cancer; gut disease;
 KW degenerative disorder; nervous system disorder; Parkinson's disease;
 KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
 KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
 KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
 KW therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9953058-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 02-APR-1999; 99WO-US007417.
 XX
 PR 15-APR-1998; 98US-00060939.
 XX
 PA (GETH) GENENTECH INC.

XX De Sauvage FJ, Carpenter DA;
 PI MPI; 1999-620428/53.
 XX
 PT New isolated human patched-2 gene, used to develop products for treating,
 PT e.g. cancer and Alzheimer's disease.
 XX
 PS Example 1; Page 93-96; 124pp; English.
 XX
 CC This sequence is a partial clone of DNA encoding the human patched-2
 CC (ptch-2) protein of the invention. The patched-2 polypeptides are
 CC signalling molecules, specifically for signalling and mediator molecules
 CC in the hedgehog (hh) cascade which are involved in cell proliferation and
 CC differentiation. They can be used for the treatment of disorders which
 CC are mediated at least in part by hh, especially Dhh, e.g. testicular
 CC cancer. They can also be used for treating degenerative disorders of the
 CC nervous system, e.g. Parkinson's disease, memory deficits, Alzheimer's
 CC disease, Lou Gehrig's disease, Huntington's disease, schizophrenia,
 CC stroke and drug addiction. Patched-2 agonists can be used to treat gut
 CC diseases, bone diseases, skin diseases, diseases of the testis (including
 CC infertility), ulcers, lung diseases, diseases of the pancreas, diabetes,
 CC and osteoporosis. Antagonists or agonists of patched-2 may be used for
 CC treating disorders or creating a desirable physiological condition
 CC effected by blocking hh signalling, especially Dhh signalling, e.g.
 CC contraception or infertility treatment. The products can also be used for
 CC detection, diagnosis, drug screening and production of transgenic animals
 XX
 SQ Sequence 4004 BP; 724 A; 1330 C; 1100 G; 850 T; 0 U; 0 Other;
 Alignment Scores: Length: 4004
 Pred. No.: 2e-291 Matches: 847
 Score: 3955.00 Conservative: 2
 Percent Similarity: 65.81% Mismatches: 10
 Best Local Similarity: 65.66% Indels: 434
 Query Match: 63.06% Gaps: 10
 DB: 2
 US-09-990-046-2 (1-1203) x AAZ31728 (1-4004)
 QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuLeuGlnThrAlaArg 120
 Db 11 CCGGAGAAAGCTGGGGAGGAGGCTGCATACCTCTCAGATGCTGTATACAGCCGACGC 70
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 Db 71 CAGAGGGAGAGAACATCTCACCCGGAAGCACTTGGCTCCACCTCCAGGAGACCCCTC 130
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 Db 131 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCTCTGGGATTTGAACMAATCTGC 190
 QY 161 TyrLysSerGlyValProLeuLeuGluAsnGlyMetIleGlnTrpMetIleGluLysLeu 180
 Db 191 TACAAGTCAGAGTTCCTTATTGAAATGGAATGATTCAGCGGATGATGTGAGAAGCTG 250
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
 Db 251 TTTCCGGTGGTGAATCTCACCCCTCGACTCTCTGGGAGGAGCCAACTCCAAAGG 310
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
 Db 311 GGCTCCGCTACCTCGCGCT----- 330
 QY 221 LeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 Db 330 ----- 330
 QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
 Db 330 ----- 330
 QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280

Db 331 -----|||||-----CCCAATGTGGCTACGAGCTGAGT 354
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db 355 GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 414
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 415 GGCATGGCCAGAGACCCCAAGGAGAGCTGTGAGGGCAGAGGCCCTGCGAGACACCTTC 474
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 475 TTGCTGATGAGTCCCGCCAGCTGTACGAGCAATTCGGGGTGACTATGACACATGAC 534
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal 360
Db 535 ATTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGTACAAGCCTGGCAGCGCGCTTTGTG 594
Qy 360 -----|||||----- 360
Db 595 CAGTCTGGTATGGACAAGGACAGGGGGGTGCCCTGAGGCCATTCCTCTCTGCCCCCT 654
Qy 361 -----GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGly 374
Db 655 CCTATCCACCCCTGTTCTCCAGCTGGCCAGGAGGCCCTGCCTGAGACGCTTCCAGCA 714
Qy 374 nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
Db 715 GATCCATGSCCTTCTCTCCACCAACCTTGGATGACATCTGTCATGCGTTCCTGAAGTCAG 774
Qy 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet----- 405
Db 775 TGCTGCCCGTGTGGAGGCTAATCTGCTCATGTTGGTCTTGACACCTGGCACTTGCC 834
Qy 405 -----|||||----- 405
Db 835 CCCACCCCACTCCAAACAGTGCACCCCTGGGGAGCCCTGAGACTGCCCTTTCCCCCC 894
Qy 406 -----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
Db 895 ACAGCTGGCCTATGCTGTGTGACCATGCTGCGGTGGGACTGGGCCCACTCCAGGGTTC 954
Qy 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCTTTGCCGGGGTACTGCTGGTGGCCCTGGCGGTGGCCCTCAGGCCCTTGGGCTCTG 1014
Qy 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr----- 456
Db 1015 TGCCCTGCTCGGCATCACCTTCAATGTGTCACATACCAGGTACGCCAGGACTGCAGGGC 1074
Qy 457 -----|||||-----G 457
Db 1075 AGACTCAGTGCAGTCACAGGCTTCACGGGTCTCAGCTGCCCGCTCCTCTGCGCCCTCC 1134
Qy 457 lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
Db 1135 AGTGCTGCCCTTCTTGACTCTGGGAATCGCGTGGATGACGTATTCTCCTGCGCGCATG 1194
Qy 477 laPheThrGluAlaLeuProGlyThr----- 485
Db 1195 CCTTCACAGAGGCTCTGCTGTGGCAACCCCTCCAGGTGGGGCCTTGTCCCCCAGGGCTCA 1254
Qy 485 -----|||||----- 485
Db 1255 TCTGAGCAGCTCAGCTTACTGGTAAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA 1314
Qy 485 -----|||||----- 485
Db 1315 ATGAACCTCGGTGCTCTTGTCCCATGTGTAAACAGGGGAAATAATAGTGTGTCTCT 1374
Qy 485 -----|||||----- 485

Db 1375 AAGGTTATTGTTGGATCAGTGAAGTAACCTCAAGTTGAATGCTTAGAACAGCCCATCAT 1434
Qy 485 -----|||||----- 485
Db 1435 ACGTACATGTTACCCCAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCACCC 1494
Qy 485 -----|||||----- 485
Db 1495 CAAATTCTCAGCGCTCCCTTCACTCCACTTTGACAGCGGCCCTCCCTTGTGACCTGAGG 1554
Qy 486 -----ProLeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyT 500
Db 1555 GCAGTCCCACTCTGCTCTGG--CAGGAGGCATGGCGGAGTGTCTGACGGCAGCGGCA 1613
Qy 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValp 520
Db 1614 CCAGTGTGTACTACATCATCAACAACATGGCGGCTCTCTCATGCTGCTCGTCTC 1673
Qy 520 rIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCCTTCTCC----- 1699
Qy 540 alaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgHisCys 559
Db 1700 -----CTACAGCCTGGACCTTACGGCGGCCACTGC 1730
Qy 560 GlnArgLeuAspValLeuCysCysPheSer----- 569
Db 1731 CAGCGCCTTGATGTGCTCTGCTCTC--CAGTACTGCTGCGCCAGCCCTTCTCCT 1789
Qy 569 -----|||||----- 569
Db 1790 CCCGTGACCCACGCCAGCTGTCCCTCACAGCAITTCAGGCACAGACTGTGATCCA 1849
Qy 570 -----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCTGCCCCAGAGCTG 1909
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGGACGGGACAGTACACAGTGGGCATTCGCCACCTCACTGCCACAGTTCAAGCCTTACC 1969
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCAGCATGTGTCACCATCTGCTCCCAAGCCCACTGGTG 2029
Qy 625 ProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTACGCCCTGGAGGCTCCACAGGGAC 2089
Qy 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTCTAGGCCAGGAGGAGAGCAAGGCAGAGCCCTGCAAGTCCCTGCCCTGTGCC 2149
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
Db 2150 CGCTGAAATCTTGCCCAATTCGCCCGCTATCAGTTTGCCTGCTGCTGCCAGTCACAT 2209
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2210 GCCAAGGCCATCTGCTGCTGCTGCTTCTTCTGGGCTGAGCCTCTACGGAGCC 2269
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGGTCAAGAGCGCTGCGCTGACGGATGTGTCCTCGGGGCCACCAAGAGCAT 2329
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCTCTCTCAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGTGGCCCTGTGTGCCAG 2389
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2390 GGTGGCTTTGACTACGCCCACTCCCAACGCGCCCTCTTTGATCTGACGAGCCTTCAGT 2449

QY 765 SerLeuIysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
 Db 2450 TCCCTCAAGGGGCTGCTGCCCCACCCAGCCACCCCGACCTCGCTGCATAT 2509
 QY 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
 Db 2510 TACCGCAACTGGCTACAGGAATCCAGCTGCCTTTGACAGGACTGGCTTCTGGGCGC 2569
 QY 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
 Db 2570 ATCACCGCCACTCGTATCCGCAATGGCTCTGAGATGGGGCCCTGGCTACAGCTGCTC 2629
 QY 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer----- 837
 Db 2630 ATCCAGACTGGAGACGCCAGGAGCCCTCTGGATTTACAGCCAGGTGGGAGGGCTGGAG 2689
 QY 837 ----- 837
 Db 2690 GGGTCCACTAGTACAGGGGCTGCAGGCTCTCTGGGCCAGGCTTCAGCCCTCTCTGCCT 2749
 QY 838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
 Db 2750 CTGCAGCTGACCAAGAAAGCTGGTGACAGAGAGGACTGATTCACCCGAGCTCTTC 2809
 QY 857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
 Db 2810 TACATGGGGTGTACCGTGTGGTGAGCAGTGACCCCTGGGTGGGAGGCTTCACAGGCC 2869
 QY 877 AspPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
 Db 2870 AACTTCTACCCCCACCTCTCTGAATGCTGCACGACAAATACGACACCCAGGGGAGAAC 2929
 QY 897 LeuArg----- 898
 Db 2930 CTTGGCAGTGAATTTGGGGGAGCTCGGCAAGAGCTCAGCTCGGCCACACAGCCCT 2989
 QY 898 ----- 898
 Db 2990 GAGCTGAGGCCCTGCCACTCTGCCCGGTGCTACGCGCTGTCCCTCTCTCTCTCTCTC 3049
 QY 899 -----IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
 Db 3050 CCTTCCCTCCCTCCACAGTCCCGCCAGCTCAGCGCTTGAGATTGCCAGTTCCCTT 3109
 QY 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
 Db 3110 CCTGCTCGGCTCCAGAAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGCGCCGGC 3169
 QY 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
 Db 3170 AGCATGCCAGAGCGCCGACGCTGGGTGTCACGCTTACCCAGCGGCTCCCTCTCTCT 3229
 QY 952 upheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
 Db 3230 CTTCTGGGAACAGTATCTGGGCTCGCGCGTGTCTCTGCTGGCCCTGTGCTATCTGCT 3289
 QY 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuLeuAsnProThrAlaGlyLeuI 992
 Db 3290 GGTGTGACTTCTCTGCTGTCTGCTCTCTCAACCCCTGGAGCGCTGCGCTCAT 3349
 QY 992 e----- 992
 Db 3350 AGTGAGTGTGAGAGTGGGAGACAGACACCCCTTCCCTGCCCGAGCTGTCTAT 3409
 QY 993 -----ValLeuValLeuAlaMetM 999
 Db 3410 CCTCTCTGCCAGGACCTCTGTGAGCCCTGTCTCTCCCTCAGGTGTCTGTCTGTGCGATGA 3469
 QY 999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProv 1019
 Db 3470 TGACAGTGGAACTCTTTGGTATCATGGGTTCCTCTGGGATCAAGCTGAGTCCATCCCG 3529

1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
 3530 TGTGATCTCTGTGGCTCTGTAGGATTGGCTGTAGTTACAGTCCAGTGGCTCTGG 3589
 1039 lyPheLeuThrThrGlnGly 1045
 3590 TGAGCACGGGACCCCGGG 3609

RESULT 8
 AAD31580
 ID AAD31580 standard; cDNA; 4004 BP.
 XX
 AC AAD31580;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human patched-2 (Ptch-2) cDNA clone 3A.
 XX
 KW Human; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
 KW cytostatic; testicular cancer; hedgehog protein signalling; clone 3A; ss.
 XX
 OS Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT primer_bind 30..50
 FT /*tag= a
 FT /bound_moiety= "RACE 6 PCR primer"
 FT primer_bind
 FT /*tag= b
 FT /bound_moiety= "RACE 5 PCR primer"
 XX
 PN US6348575-B1.
 XX
 PD 19-FEB-2002.
 XX
 PF 15-APR-1999; 99US-00293505.
 XX
 PR 15-APR-1998; 98US-0081884P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI De Sauvage F, Carpenter DA;
 XX
 DR WPI; 2002-215260/27.
 XX
 PT Native human patched-2 polypeptide for treating disorders caused by
 PT Hedgehog protein signaling such as testicular cancer, and for screening
 PT cDNA libraries.
 XX
 PS Example 1; Fig 10; 82pp; English.
 XX
 CC The invention relates to an isolated sequence comprising a native human
 CC patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
 CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
 CC cell proliferation and differentiation. The isolated sequence is useful
 CC for the treatment of disorders which are linked to hedgehog, especially
 CC Desert hedgehog expression, such as testicular cancer. It may also be
 CC used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
 CC homologues, and to diagnose whether a disorder is driven by Ptch-2 or
 CC Hedgehog protein signalling. The present sequence is human patched-2
 CC (Ptch-2) cDNA clone 3A
 XX
 SQ Sequence 4004 BP; 724 A; 1330 C; 1100 G; 850 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2e-291 Length: 4004
 Score: 3955.00 Matches: 847
 Percent Similarity: 65.81% Conservative: 2
 Best Local Similarity: 65.66% Mismatches: 10
 Query Match: 63.06% Indels: 434
 DB: 6 Gaps: 10

US-09-990-046-2 (1-1203) x AAD31580 (1-4004)

QY	101	LysGluLysLeuGlyGluGluAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg	120	QY	406	-----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe	424
Db	11	CGGAGAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTATACAGACCGACGC	70	Db	895	ACAGCTGGGCTATGCTGTGTGACCATGCTGCGGTGGAGCTGCGCCAGTCCCGAGGTTTC	954
QY	121	GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu	140	QY	424	rValGlyLeuAlaGlyValValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy	444
Db	71	CAGAGGGAGAGAACATCTCCACCCGGAAGCACTTGGCCCTCCACCTCCAGGAGCCCTC	130	Db	955	CGTGGGCTTGGGGGTACTGCTGGTGGCCCTGGCGGTGGCTCAGGCTTGGGCTCTG	1014
QY	141	ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys	160	QY	444	sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr-----	456
Db	131	ACTGCCAGTAAAGTCCCAAGTATCACTCTATGGGAAGTCCCTGGGATTTGAACAAATCTGC	150	Db	1015	TGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTACGCCAGGACTGCAGGC	1074
QY	161	TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu	180	QY	457	-----G	457
Db	191	TACAAGTCAGAGTTCCTCCCTTATTGAAATGGAATGATTGAGCGGATGATTGAAAGCTG	250	Db	1075	AGACTCAGTGCCAGTCACCAGGCTTCACGGGTCTCAGGTGCCCGCTCTCTGCCCCCTCC	1134
QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly	200	QY	457	lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA	477
Db	251	TTTCCGTGGGTGATCTCACCCTCCCTGACTGCTCTCTGGAGGAGGCCAACTCCAAAGG	310	Db	1135	AGGTGCTGCCCTTCTTGACTCTGGGANTCGGCGTGGATGACGTATCTCTGCTGGCGCATG	1194
QY	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220	QY	477	laPheThrGluAlaLeuProGlyThr-----	485
Db	311	GGCTCCGCTACCTGCGCT-----	330	Db	1195	CTTTCACAGAGGCTCTGCTGGCACCCCTCTCCAGGTGGGGCCTTGTCCCCCAGGGCTCA	1254
QY	221	LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240	QY	485	-----	485
Db	330	-----	330	Db	1255	TCTGAGGACGCTCAGCTTACTGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA	1314
QY	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys	260	QY	485	-----	485
Db	330	-----	330	Db	1315	ATGAACCTCGGTGCTCTTGTCCCCCATGTGTAAACAGGGGAATAATAGTGTGTCTCT	1374
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280	QY	485	-----	485
Db	331	-----CCCAATGTGGCTCAGAGCTGAGT	354	Db	1375	AAGGGTTATTGTTGGATCAGTGAAGTAACTCAAGTTGAATGCTTAGAACAGGCCCATCAT	1434
QY	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuLeuGly	300	QY	485	-----	485
Db	355	GGGGGTGCCATGGCTCTCCCAAAATTCACTGCTGGCAGGAGAAATTGCTGTGGGA	414	Db	1435	ACGTACATGGTACCCCAATAAATGCTAGCCACTGTGTATGACTGCCCCCCTCTGCACCC	1494
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320	QY	485	-----	485
Db	415	GGCATGGCAGACACCCCAAGAGAGCTGCTGAGGCGAGGCCCTTGACAGACCTTC	474	Db	1495	CAAGTTCCTGAGCCTCCCTTCACTCCACTTTGACAGGCCCTCCCTCTGTGACCTGAGG	1554
QY	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340	QY	486	-----ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyT	500
Db	475	TTGCTGATGAGTCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC	534	Db	1555	GCAGGTCCCACTCTGCTCTGG-CAGGAGCGCATGGCGAGTGTCTGCAGCGCACGGCA	1613
QY	341	IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal	360	QY	500	hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP	520
Db	535	ATTGGCTGGAGTGAGGAGCAGGCAGCACAGTGTACAAGCCTGGCAGCGCGCTTTGTG	594	Db	1614	CCAGTGTGTACTACATCATCAACAACATGGCCGCTTCTCTATGGGTGCCCTCGTTC	1673
QY	360	-----	360	QY	520	roileProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV	540
Db	595	CAGGTGCTGATGACAGGACAGGGGGTGCCCTGAGGCCATTCCTCTCTGCCCCCT	654	Db	1674	CCATCCTCGGCTGCCAGCCTTCTCC-----	1699
QY	361	-----GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGly	374	QY	540	alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgHisCys	559
Db	655	CCTATCCACCCCTGTTTCTCCAGCTGGCCCGAGGAGCCCTGCTGAGAACGCTTCCAGCA	714	Db	1700	-----CTACAGCCTGGACCTACGGCGGCGCCACTGC	1730
QY	374	nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe	394	QY	560	GlnArgLeuAspValLeuCysCysPheSer-----	569
Db	715	GATCCATGCCCTTCTCTCCACCACTCCGTGATGATCCTGATGCGTCTCTGAAGTCAG	774	Db	1731	CAGCGCTTGTGATGTCTGCTGCTTCTC-CAGGTACTGCTGCGCCCCCAGGCCCTTCCCT	1789
QY	394	rAlaAlaArgValValGlyTyrLeuLeuMet-----	405	QY	569	-----	569
Db	775	TGCTGCCCGGTGGTGGAGGCTATCTGCTCATGGTGGGTCTTGACACTGGCACCTGGCACCT	834	Db	1790	CCCGTGACCCAGCCAGCCTGCTCCCTCACCAGCATTTTCAAGGCACAGACCTGTCTATCCA	1849
QY	405	-----	405	QY	570	-----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu	594
Db	835	CCCAACCCCACTCCAACAGTGCACCCCTTGGGAGGCCCTGAGACTGCTTTCCTCCCT	894	Db	1850	CTCTCTACTCTTCTTCAGTCCCTGCTCTGCTCAGGTGATTTCAGATCCTGCCCCAGGAGCTG	1909

QY 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
DB 1910 GGGAGCGGACAGTACCAGTGGGCAATGGCCACCTCACTGCCAGTTCAAGCCTTTACC 1969
QY 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProGlnAlaHisLeuVal 624
DB 1970 CACTGTGAAGCCAGCAGCCAGCATGTGTGTCACCATCTGCTCCCAAGCCACCTGGTG 2029
QY 625 ProProSerSerProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
DB 2030 CCCCCCCTTCTGACCCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACAGGGAC 2089
QY 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
DB 2090 CTTCTAGGCCAGGAGGAGGAGACAGCAGAGCCAGCTTCAAGTCTCCCTGGCTGTGCC 2149
QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
DB 2150 CGCTGGAATCTTGCCCAATTTGCCCGCTATCAGTTTCCCGCTGTGCTCCAGTCACAT 2209
QY 685 AlaLysAlaIleValLeuValPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
DB 2210 GCCAAGGCCATCTGTGCTGGTCTTGTGGTCTTCTTGGGCTTGAGCCTCTACGGAGCC 2269
QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
DB 2270 ACCTTGTGTCAAGAGCGCCTGGCCCTGACGGATGTGGTCTCGGGCACCAAGGACAT 2329
QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
DB 2330 GCCTTCTGAGCCGCCAGCTCAGTACTCTCTCTGTACAGGTTGGCCCTGTGACCCAG 2389
QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
DB 2390 GGTGGCTTTGACTACGCCCACTCCCAAGCGCCCTCTTTGATCTGCACCAAGCCTTCAGT 2449
QY 765 SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
DB 2450 TCCCTCAAGCGGTGTGTGCCCCACCGCCACCCAGCCAGCCACCTGGCTGCACTAT 2509
QY 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
DB 2510 TACCGCACTGGCTACAGGGAATCCAGGCTGCTTTGACCAAGACTGGGCTCTGGCGCC 2569
QY 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeu 824
DB 2570 ATCACCAGCCACTCGTACCCCAATGGCTCTGAGATGGGCGCCCTGGCCTTCAAGCTGCTC 2629
QY 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer 837
DB 2630 ATCCAGACTGGAGACGCCAGGAGCCTCTGGATTTTACGCCAGGTGGGAGGGCTGGAG 2689
QY 837 837
DB 2690 GGGTCCACTAGTACAGGGGCTGACGGGCTCTCTGGGCCAGGCCCTTACGCCCTCTCTGCCT 2749
QY 838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
DB 2750 CTCACCTGACCAACAGGAGCTGGTGACAGAGGAGCTGATTCACCCGAGCTCTTC 2809
QY 857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaLaserGlnAla 876
DB 2810 TACATGGGCTGACCGTGTGGGTGAGCAGTGACCCCTGGGTCTGGCAGCCTCACAGGCC 2869
QY 877 AsnPheTyrProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
DB 2870 AACTTCTACCCCCACCTCTCTGAATGGCTGACAGCAAAATACGACACCAAGCGGGAGAAC 2929
QY 897 LeuArg 898
DB 2930 CTTGCGAGTCAGTCTTGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCACACAGCCCT 2989
QY 898 898

DB 2990 GAGCTGAGGCCCTGCCCACTCTGCCCGGTGCTCACGCCCTTCCCTCTCCCTCTTCTC 3049
QY 899 -----IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
DB 3050 CTTTCCCTCCCTCCCACTGCGCGCAGCTCAGCCCTGGAGTTTCCCAAGTTCCCTT 3109
QY 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
DB 3110 CCTGCTGCTGGGCTCCAGAGACTGTCAGACTTTGTGGAGGCCATCCAGGGGGCCCGGC 3169
QY 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
DB 3170 AGCATGGCAGAGCGCGCCAGGCTGGGTGTCAGCCTACCCACAGCGCTCCCCCTTCT 3229
QY 952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
DB 3230 CTTCTGGGAACAGTATCTGGGCTTGGGCGCTGCTTCTGCTGCGCCCTGTCATCTGCT 3289
QY 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuI 992
DB 3290 GGTGTGACATTTCTGCTGCTGCTGCTGCTTCTCAACCCCTGGACGCTGCGCTCAT 3349
QY 992 e----- 992
DB 3350 AGTGAGTGTCTGAGGAGTGGGACAGACACCCACCCCTTCCCTGCCCGCCTGTCTCAT 3409
QY 993 -----ValLeuValLeuAlaMetM 999
DB 3410 CCCTCTGCCAGGAGCCCTCTGTAGCCCTGTCTCCCTCAGGTGCTGCTGCGCATGA 3469
QY 999 eThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
DB 3470 TGACGTGGAACTCTTTGGTATCATGGGTTTCTGGGCATCAAGCTGAGTGCCATCCCG 3529
QY 1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
DB 3530 TGTGTATCTTGTGGCTCTGTAGGATTTGGCGTTGAGTTTACAGTCCACGCTGCTGG 3589
QY 1039 lypheLeuThrThrGlnGly 1045
DB 3590 TGAGCACGGGCACCCCGGG 3609
RESULT 9
ABX15923
ID ABX15923 standard; cDNA; 4004 BP.
XX
AC ABX15923;
XX
DT 02-APR-2003 (first entry)
XX
DE Human partial cDNA for patched-2 from brain.
XX
KW Human; patched-2; Dhh signalling; proliferation; differentiation; ss;
KW chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
KW basal cell carcinoma; neurodegenerative disorder; memory deficit;
KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
KW bone disease; skin disease; testicular disease; ulcer; lung disease;
KW pancreatic disease; diabetes; osteoporosis; desert hedgehog.
XX
OS Homo sapiens.
XX
PN US2002156245-A1.
XX
PD 24-OCT-2002.
XX
PF 20-NOV-2001; 2001US-00990046.
XX
PR 15-APR-1998; 98US-0081884P.
PR 15-APR-1999; 99US-00293505.
XX
PA (GETH) GENENTECH INC.

Db	1255	TCTGAGCAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTAGCCTTGGGCTGCTA	1314	Db	2270	ACCTTGGTCAAGCGGCTTGGCCCTGACGGATGTGTGCTCGGGGCAACAAGGAGCAT	2322
QY	485	-----	485	QY	725	AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln	744
Db	1315	ATGAACCTCGGTGGCTCTTGTCCCATGTGTAAACAGGGGAAATAATAGTGTCTGTGCCT	1374	Db	2330	GCCTTCTTGAGGGCCAGCTCAGGTACTTCTCCCTGTACAGAGTGGCCCTGGTGACCCAG	2389
QY	485	-----	485	QY	745	GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer	764
Db	1375	AAGGGTTATTGTTGGATCAGTGAAGTAACCAAGTTGAATGCTTAGACAGGCCATCAT	1434	Db	2390	GGTGGCTTTGACTACGCCCACTCCAAACGGGCCCTCTTTGATCTGCACACGAGCGCTTCAGT	2449
QY	485	-----	485	QY	765	SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTlpLeuHisTyr	784
Db	1435	ACGTACATGTTACCAATAAATGCTAGCCACTGTGTATGACTGCCCAACCTCTGCACCC	1494	Db	2450	TCCCTCAAGGGGGTGTGCCCCACCGGCCACCCAGGCACCCCGACCTGGCTGCACTAT	2509
QY	485	-----	485	QY	785	TyrArgAsnTlpLeuGlnGlyLeGlnAlaAlaPheAspGlnAspTlpAlaSerGlyArg	804
Db	1495	CAAGTTCCTGAGCCTCCCTTCACTCCACTTTGACACGGCCCTCCCTTGTGACCTGAGG	1554	Db	2510	TACCCAACTGGCTACAGGGAATCCAGCTGCCTTTGACACAGACTGGGGTTCTGGGGCGC	2569
QY	486	-----	486	QY	805	IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu	824
Db	1555	GCAGGTCCCACTCTCTCTGG-CAGGAGCGATGGGCGAGTGTCTGCAGCGCACGGCA	1613	Db	2570	ATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGCCCTGGCCCTACAAGCTGCTC	2629
QY	500	hSerValValLeuThrSerIleAsnMetAlaAlaPheLeuMetAlaAlaLeuValP	520	QY	825	IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer	837
Db	1614	CCAGTGTCTACTCATCTCATCAACATGCGCGCCTTCTCATGGCTGCCCTCGTTC	1673	Db	2630	ATCCAGACTGGAGACGCCAGAGCCTCTGGATTTCAGCCAGGTTGGGAGAGGCGCTGGAG	2689
QY	520	xrIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV	540	QY	837	-----	837
Db	1674	CAATCCCTCGCTGGAGCTTCTCC-----	1699	Db	2690	GGGTCCACTAGTACAGGGGCTGAGGCTCTCTGGGCCAGGCTTCAGCCCTCTCTGCCT	2749
QY	540	AlaAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgHisCys	559	QY	838	---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProGluLeuPhe	856
Db	1700	-----CTACAGCCTGGACCTACGGCGCGCCACTGC	1730	Db	2750	CTGCAGCTGACCACAAAGAAAGCTGGTGGACAGAGAGGACTGATTCCACCCGAGCTCTTC	2809
QY	560	GlnArgLeuAspValLeuCysCysPheSer-----	569	QY	857	TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla	876
Db	1731	CAGCGCTTGATGTCTCTGTCTGTCTTC-CAGGTACTGCTGGCGGCCAGCCCTTCCT	1789	Db	2810	TACATGGGGCTGACCGTGTGGTGAGCAGTGACCCCTGGGTCTGGCAGCTCACAGGCC	2869
QY	569	-----	569	QY	877	AsnPheTyrProProGluTyrPleuHisAspLysTyrAspThrThrGlyGluAsn	896
Db	1790	CCCGTGACCCAGCGAGCCTGTCCTCACACGACATTTCAAGGCACAGACCTGTCAATCCA	1849	Db	2870	AACCTTCAACCCCACTCTCTGAATGGCTGCACACAAATACGACACACCGGGGAGAAC	2929
QY	570	-----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu	584	QY	897	LeuArg-----	898
Db	1850	CTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTTCAGATCTGCCCCAGGAGCTG	1909	Db	2930	CTTCGACTGAGTCTTGGGGGAGCTCGGCAAGAGCCTCAGCTCGGCCACACAGGCCCT	2989
QY	585	GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr	604	QY	898	-----	898
Db	1910	GGGACGGACAGTACCAGTGGGCATTGCCACCTCACTGCACACAGTTCAAGCTTTTACC	1969	Db	2990	GAGCCTGAGGGCCTGCCACACTCTGCCCGCTGCTCACCGCCCTGTCTCCCTCTCTCTC	3049
QY	605	HisCysGluAlaSerSerGlnHisValValThrIleLeuProGlnAlaHisLeuVal	624	QY	899	-----IleProProAlaGlnProLeuGluPheAlaGlnPheProPh	912
Db	1970	CAGTGTGAAGCAGCAGCAGCATGTGTGCACATCTGCTGCCCTGCCCAAGCCCACTGGTG	2029	Db	3050	CCTTCCCTCCCTCCACAGTCCCGCAGCTCAGCCCTTGAGTTTGCCCAGTTCCCTT	3109
QY	625	ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644	QY	912	eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl	932
Db	2030	CCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTTGAGGGTCCACACGGGAC	2089	Db	3110	CCTGTGCTGGCTCCAGAGACTGCGAGACTTTGTGTAGGSCCATCGAGGGGCCCGGGC	3169
QY	645	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664	QY	932	aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe	952
Db	2090	CTTCTAGGCCAGGAGGAGACAAGGAGAGGCAGCTCTCAAGTCCCTGCCCTGTGCC	2149	Db	3170	AGCATGCGAGAGGCCCGCAGGCTGGGGTGCACGCCCTACCCAGGGGCTTCCCTTCCT	3229
QY	665	ArgTlpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis	684	QY	952	uPheTlpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe	972
Db	2150	CGCTGGAATCTTGCCCATTTGCCCGCTATCAGTTTGGCCGCTTGTCTCCAGTCCAT	2209	Db	3230	CTTCTGGGAAACAGTATCTGGGCCCTGCGGCGCTGCTCTCTGCTGGCGCTTCGATCCCTG	3289
QY	685	AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla	704	QY	972	uValCysThrPheLeuValCysAlaLeuLeuLeuAsnProTlpThrAlaGlyLeuIle	992
Db	2210	GCCAAAGGCCATGTGCTGGTGTCTTTTGGTGTCTTTCTGGGCCCTGAGGCTCTACGGAGCC	2269	Db	3290	GGTGTGCATTTCTCGTCTGTCTGTCTCTCAACCCCTGGAGCGCTGCGCTCAT	3349
QY	705	ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis	724	QY	992	e-----	992
Db				Db	3350		

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QY 993 -----ValleuValleuAlaMetM 999
Db 3410 CCCTCTGCCAGGAGCCCTCTGTGAGCCCTGTCCTCCCTCAGGTGCTGCTGCTGCCGATGA 3469
QY 999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLeuGlySerAlaIleProV 1019
Db 3470 TGACAGTGAACCTCTTTGATATCATGGGTTCTTGGGCATCAAGCTGAGTGCCATCCCG 3529
QY 1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
Db 3530 TGGTGATCCTTGTGGCCCTCTGTAGGCATTGGCGTTGAGTTCACAGTCCACGCTGGCTCTGG 3589
QY 1039 lyPheLeuThrThrClnGly 1045
Db 3590 TGAGACGGGACCCCGGGG 3609

RESULT 10
ID AA231729
AA231729 standard; DNA; 2082 BP.
AC AA231729;
XX 19-JAN-2000 (first entry)
XX Human patched-2 coding sequence partial clone 16.1.
XX Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
XX cell proliferation; cell differentiation; testicular cancer; gut disease;
XX degenerative disorder; nervous system disorder; Parkinson's disease;
XX memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
XX Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
XX infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
XX therapy; ss.
XX Homo sapiens.
XX WO9553058-A1.
XX 21-OCT-1999.
XX 02-APR-1999; 99WO-US007417.
XX 15-APR-1998; 98US-00060939.
XX (GETH ) GENENTECH INC.
XX De Sauvage FU, Carpenter DA;
XX WPI; 1999-620428/53.
XX New isolated human patched-2 gene, used to develop products for treating,
XX e.g. cancer and Alzheimer's disease.
XX Example 1; Page 96-97; 124pp; English.
XX This sequence is a partial clone of DNA encoding the human patched-2
XX (ptch-2) protein of the invention. The patched-2 polypeptides are
XX signalling molecules, specifically for signalling and mediator molecules
XX in the hedgehog (hh) cascade which are involved in cell proliferation and
XX differentiation. They can be used for the treatment of disorders which
XX are mediated at least in part by hh, especially Dhh, e.g. testicular
XX cancer. They can also be used for treating degenerative disorders of the
XX nervous system, e.g. Parkinson's disease, memory deficits, Alzheimer's
XX disease, Lou Gehrig's disease, Huntington's disease, schizophrenia,
XX stroke and drug addiction. Patched-2 agonists can be used to treat gut
XX diseases, bone diseases, skin diseases, diseases of the testis (including
XX infertility), ulcers, lung diseases, diseases of the pancreas, diabetes,
XX and osteoporosis. Antagonists or agonists of patched-2 may be used for
XX treating disorders or creating a desirable physiological condition
XX effected by blocking hh signalling, especially Dhh signalling, e.g.
XX contraception or infertility treatment. The products can also be used for
XX detection, diagnosis, drug screening and production of transgenic animals

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XX SQ Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.82e-248 Length: 2082
Score: 3387.00 Matches: 656
Percent Similarity: 96.33% Conservative: 1
Best Local Similarity: 96.19% Mismatches: 3
Query Match: 54.00% Indels: 23
DB: 2 Gaps: 2
US-09-990-046-2 (1-1203) x AA231729 (1-2082)
QY 1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db 8 ATGACTCGATCGCGCCCTCAGAGAGCTGCCCGAGTTACACACCCCGAGTCTGAACC 67
QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db 68 GCAGACCCAGATCCTAGCTGGGAGCTGAAGGCTCCACTCTGGCTTCGTCTACTTC 127
QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db 128 CAGGCGCTGCTCTTCTCTGGGATGGGGATCCAGAGACATTGTGGCAAGTGTCTTT 187
QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db 188 CTGGGACTGTGGGCTTTGGGGCTTGGCATTTAGTCTCCGATGGCCATTATTGAGACA 247
QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db 248 AACTTGAACAGCTCTCTGGGTAGAAAGTGGGACGCGGTGAGCCAGGAGTGCATTACACC 307
QY 101 LysGluLysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db 308 AAGGAGAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTGTATACACCGCAGCC 367
QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
Db 368 CAGGAGGAGAGAAATCCTCACACCCGAGACCTTGGCCCTCCACCTCCAGGAGCCCTC 427
QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 428 ACTGCCAGTAAAGTCCAAAGTATCATCTATGGGAAGTCTTGGGATTTGAACAAATCTGC 487
QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db 488 TACAAGTCAGAGATTCCCTTTTGAANAATGGAATGATTGAGTGGATTTGAGAAGCTG 547
QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db 548 TTTCCGTGCGTGATCTCTCACCCCTCGACTGCTTCTGGGAGGAGGAGCAACTCCAGGG 607
QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db 608 GGCTCCGCTACCTCGCCCGCCCGGATATCATCAGTGGACCAACCTGGATCCAGAGCAG 667
QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 668 CTGCTGGAGAGCTGGGTCTCTTGGCTTCCCTTGGGGCTTCGGGAGCTGTAGACAAG 727
QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
Db 728 GCACAGTGGGCCAGGCTACGTGGGGCGGCCCTGTCTGCACCTGATGACCTCCACTGC 787
QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 788 CCACCTAGTGGCCCAACCATCATCAGCAGCAGGCTCCCAATGTGGCTCAGAGCTGAGT 847
QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuLeuGly 300
Db 848 GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCATGGCAGGAGAAATGTGCTGCTGGGA 907

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QY 301 GlyMetAlaArgAspProGlnGlyLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 908 GGCATGGCCAGAGACCCAGGAGAGCTGCTGAGGCGAGAGCCCTGCAGAGACACCTTC 967
QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 968 TTGCTGATGAGTCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027
QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal 360
Db 1028 ATTGGCTGGAGTGAGGAGCAGCCAGCAGCAGTGTCTACAGGCTGTGCAGCGCGCTTTGTG 1087
QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db 1088 CAGCTGGCCAGGAGGCCCTGCCCTGAGAACCTTCCAGCAGATCCATGCTTCTCCTCC 1147
QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db 1148 ACCACCCTGGATAACATCTCGATGCTTCTCTGAAGTCAGTGTGCTGCCCGTGTGGGA 1207
QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1208 GGCTATCTGCTCATGCTGGCCATGCTGCTGTGACCATCTGCGGTGGGACTGGGCCCGAG 1267
QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1268 TCCAGAGGTTCCGTGGGCTTTGCCGGGTACTGCTGTGGCCCTTGGCGGTGGCTCAGGC 1327
QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1328 CTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCC 1387
QY 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1388 TTTCTGGCTCTGGGAATCGGCGTGGATGACATTTCTCTGCTGGCGCATGCCCTCACAG 1447
QY 481 AlaLeuProGlyThrProLeuGlnArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1448 GCTCTGGCTGGACCCCTCTCCAGAGCGCATGGCGAGTGTCTGCAGCGCAGCGGCACC 1507
QY 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1508 AGTGTCTGACTCACATCATCAACAACATGGCGCTTCTCTCATGCTGCCCTGCTGCC 1567
QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1568 ATCCCTGGCTGCGAGCCTTCTCTTACAGCC----- 1599
QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
Db 1600 -----ATCCTCAGCTGGACCTTACGGCGCGGCACCTGCCAG 1635
QY 561 ArgLeuAspValLeuCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1636 CGCCTTGATGTCTGTGCTTCTCCAGTCCCTGCTCTGCTCAGTGATTCAGATCCTG 1695
QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1696 CCCCAGGAGCTGGGGAGCGGACAGATACAGTGGGCATTGGCCACCTCAGTGCACACATT 1755
QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
Db 1756 CAGGCTTTTACCATCTGTGAGCCAGCAGCCAGCATGTGGTCACCATCTGCTCCCTCCCA 1815
QY 621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 1816 GCCACCTGGTGGCCCCACCTTCTGACCCACTGGGCTCTGAGCTTTCAGGCCCTGGAGGG 1875
QY 641 SerThrArgAspLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysIysSer 660
Db 1876 TCCACAGGGACCTTCTTAGGCCAGGAGGAGAGCAAGGAGAGGAGCTTGCAGTCC 1935
QY 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
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Db 1936 CTGCCCTGTGCCCTCGAATCTTCCCAT-----TTGCCCCCGAATTC 1980
QY 681 LeuGln 682
Db 1981 CTGCAG 1986
RESULT 11
AAD31581
ID AAD31581 standard; cDNA; 2082 BP.
XX
AC AAD31581;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human patched-2 (Ptch-2) cDNA clone 16.1.
XX
KW Human; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
KW cytosolic; testicular cancer; hedgehog protein signalling; clone 16.1;
KW ss.
XX Homo sapiens.
XX
FN US6348575-B1.
XX
PD 19-FEB-2002.
XX
PF 15-APR-1999; 99US-00293505.
XX
PR 15-APR-1998; 98US-0081894P.
XX
PA (GETH ) GENENTECH INC.
XX
PI De Sauvage F, Carpenter DA;
XX
DR WPI; 2002-215260/27.
XX
PT Native human patched-2 polypeptide for treating disorders caused by
PT hedgehog protein signaling such as testicular cancer, and for screening
PT cDNA libraries.
XX
PS Example 1; Fig 11; 82pp; English.
XX
CC The invention relates to an isolated sequence comprising a native human
CC patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC cell proliferation and differentiation. The isolated sequence is useful
CC for the treatment of disorders which are linked to Hedgehog, especially
CC Desert hedgehog expression, such as testicular cancer. It may also be
CC used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC hedgehog protein signalling. The present sequence is human patched-2
CC (Ptch-2) cDNA clone 16.1
XX
SQ Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.82e-248 Length: 2082
Score: 3387.00 Matches: 656
Percent Similarity: 96.33% Conservative: 1
Best Local Similarity: 96.19% Mismatches: 3
Query Match: 54.00% Indels: 23
DB: Gaps: 2
US-09-990-046-2 (1-1203) x AAD31581 (1-2082)
QY 1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db 8 ATGACTCGATCGCGCCCTCAGAGAGCTGCCCGAGTTACACACCCAGCTCGAACC 67
QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db 68 GCAGCACCAGATCTAGCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 127
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QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 Db 128 CAGGGCCTGCTCTCTCTGGGATGGGGATCCAGAGACATTGTGGCAAAAGTGTCTTT 187
 QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
 Db 188 CTGGGACTCTGGCCCTTTGGGGCCCTGGGCATTAGGTCTCCGATGGCCATTATTAGACA 247
 QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
 Db 248 AACTTGGAAACAGCTCTGGGTAGAGTGGGAGCCGGGTGAGCAGAGCTGCATTACACC 307
 QY 101 LysGluLysLeuGlyGluGluAlaIleTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 Db 308 AAGGAGAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCAGC 367
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 Db 368 CAGGAGGAGAGAACATCTCTCACACCCGAAGCACTTGGCCCTCCACCTCCAGGAGCCCTC 427
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 Db 428 ACTGCCAGTAAAGTCCAAAGTATCACTCTATGGGAGTCTCTGGGATTTGAACAAATCTGC 487
 QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
 Db 488 TACAGTTCAGAGTTCCTCCCTTTATTGAAATATGGAATGATTGAGTGGATGAGAAAGCTG 547
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
 Db 548 TTTCCGTGCGTGTATCTCACCCCTCGACTCTCTGGGAGGAGCAAACTCCAAAGGG 607
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpAsnLeuAspProGluGln 220
 Db 608 GGCTCCGCCCTACCTGCCCGCCCGCCGGATATCCAGTGGACCAACTGGATCCAGAGCAG 667
 QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 Db 727 CTGCTGAGAGAGCTGGGTCTCTTGCCTTCTGAGGGCTTCGCGGAGCTGCTAGACAAG 727
 QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
 Db 728 GCACAGTGGGCCAGGCTAGTGGGGCGGCCCTGTCTGCACCTGTATGACCTCCACTGC 787
 QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
 Db 788 CCACCTAGTCCCCCAACCATCACAGCAGCAGGCTCCCAATGTGGCTCACAGAGCTGAGT 847
 QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
 Db 848 GGGGGCTGCCATGGCTTCTCCACAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGA 907
 QY 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
 Db 908 GGCATGGCCAGAGACCCCAAGAGAGCTGTGAGGGCAGAGGCCCTCCAGAGCACCTTC 967
 QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
 Db 968 TTGCTGTATGAGTCCCCCGCCAGCTGTACAGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027
 QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
 Db 1028 ATTGCTGAGTGGAGGAGCAGCCAGCAGCAGTGTCTACAAAGCTGGCAGCGGCGCTTCTGTG 1087
 QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
 Db 1088 CAGCTGGGCCAGGAGGCGCTGCTGAGAACGCTTCCAGCAGATCCATGCTCTTCTCCCTCC 1147
 QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
 Db 1148 ACCACCTGGATAACATCTCTGATGCGTCTCTGAAGTCAGTGTCTGCTGGTGGGA 1207

QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
 Db 1208 GGCTATCTGCTCATGCTGGCCCTATGCTGTGTGACCATGCTGGGTGGGACTGCGCCAG 1267
 QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
 Db 1268 TCCAGGGTTCCGTGGGCTTGGTGGGCTTGGTGGTGGGCTGGCGCTGAGGC 1327
 QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
 Db 1328 CTTGGGCTCTGGCCCTGCTCGGCATCACCTTCATGTCTGCCACTACCCAGGCTGTGCC 1387
 QY 461 PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu 480
 Db 1388 TTTCTGGCTCTGGGAATCGCGTGGATGACGTATTCTCTGCTGGCGCATGCCCTTCACAGAG 1447
 QY 481 AlaLeuProGlyThrProLeuGlnArgMetGlyGluCysLeuGlnArgThrGlyThr 500
 Db 1448 GCTCTGCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCAGGGCACC 1507
 QY 501 SerValValLeuThrSerIleAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
 Db 1508 AGTGTCTGTACATCCATCAACATGGCGCCCTTCTCATGGCTGCCCTGCTGTCCC 1567
 QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
 Db 1568 ATCCCTGCGCTGGAGCCTTCTCTTACAGCC----- 1599
 QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
 Db 1600 -----ATCCTCAGCTGGACCTACCGCGGGCGCACTGCCAG 1635
 QY 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
 Db 1636 CGCTTGTATGTCTGCTGCTTCTCCAGTCCCTGCTGCTGCTCAGGTGATTCAGATCCTG 1695
 QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
 Db 1696 CCCCAGGAGCTGGGGAGCGGAGACAGTACCAGTGGGCATTGCCACCTCTCAGTGCACAGTT 1755
 QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
 Db 1756 CAAAGCTTTACCCACTGTGAAGCAGCAGCAGCATGTGGTCCACCATCTGCTGCCCTCCCAA 1815
 QY 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
 Db 1816 GCCACCTGTGGCCCCCACCCTTCTGACCCACTGGGCTCTGAGCTCTCAGCCCTGGAGGG 1875
 QY 641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
 Db 1876 TCCACAGGAGCCTTCTAGCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1935
 QY 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
 Db 1936 CTGCGCTGTGGCGCTGGAATCTTGGCCAT-----TTGCGCCCCGGAATTC 1980
 QY 681 LeuGln 682
 Db 1981 CTGCAG 1986

RESULT 12

ABX15924
 ID ABX15924 standard; cDNA; 2082 BP.

XX AC ABX15924;

XX 02-APR-2003 (first entry)

DE Human partial cDNA for patched-2 from testis.

XX Human; patched-2; Dhh signalling; proliferation; differentiation; ss;
 KW chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
 KW basal cell carcinoma; neurodegenerative disorder; memory deficit;

KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
 KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
 KW bone disease; skin disease; testicular disease; ulcer; lung disease;
 KW pancreatic disease; diabetes; osteoporosis; desert hedgehog.

OS Homo sapiens.

XX US2002156245-A1.

PN 24-OCT-2002.

XX 20-NOV-2001; 2001US-009900046.

XX 15-APR-1998; 98US-0081884P.

PR 15-APR-1999; 99US-00293505.

XX (GETH) GENENTECH INC.

PA De Sauvage FJ, Carpenter DA;

XX WPI; 2003-182650/18.

DR New nucleic acid, useful for manufacturing a medicament for diagnosing or

PT treating a disorder that is modulated by Desert hedgehog (Dhh) signaling

PT e.g., testicular cancer.

XX Example 1; Fig 11; 85pp; English.

CC The invention relates to a new isolated nucleic acid encoding a
 CC polypeptide having patched-2 biological activity, comprises DNA having at
 CC least 95% sequence identity with a DNA molecule or its complement
 CC encoding: (a) a human patched-2 polypeptide comprising the sequence
 CC ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
 CC Deposit No. 209778 designation). Also included are a vector comprising
 CC the nucleic acid, a host cell transformed with the vector, a process for
 CC producing patched-2 polypeptides, an isolated native sequence of human
 CC patched-2 polypeptide, a chimeric molecule comprising the vertebrate
 CC patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
 CC hedgehog (Dhh) function in the Dhh signalling pathway, an agonist of
 CC patched-2 that stimulates or enhances the normal functioning of patched-2
 CC in the Dhh signalling pathway, screening for ant/agonists of patched-2
 CC and diagnosing to determine whether a particular disorder is modulated
 CC The nucleic acid is useful for manufacturing a medicament for diagnosing
 CC or treating a disorder that is modulated by Dhh signalling e.g. tumour,
 CC basal cell carcinoma, neurodegenerative disorders, memory deficit,
 CC Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
 CC Huntington's disease, schizophrenia, stroke, drug addiction, gut
 CC diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
 CC diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
 CC Patched-2 may also be used to develop male contraceptives. The gene for
 CC Patched-2 is located on human chromosome 1p33-34. The present sequence is
 CC a Human partial cDNA for patched-2 from testis

SQ Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.82e-248 Length: 2082
 Score: 3387.00 Matches: 656
 Percent Similarity: 96.33% Conservative: 1
 Best Local Similarity: 96.13% Mismatches: 3
 Query Match: 54.00% Indels: 23
 DB: 8 Gaps: 2

US-09-990-046-2 (1-1203) x ABX15924 (1-2082)

QY 1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProAlaArgThr 20
 Db 8 ATGACTCGATCGCCGCCCTCAGAGAGCTGCCCGGAGTTACACACCCCGAGCTCGAAC 67
 QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
 Db 68 GCAGCAGCCCGAGATCTTAGTGGAGGCTGAAGGCTCCACTCTGGCTTCGTCTACTTTC 127

QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 Db 128 CAGGGCCCTGCTCTTCTCTGGGATCGGGATCCAGAGACATTTGGGAAAGTGTCTTT 187
 QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleLeuThr 80
 Db 188 CTGGGACTGTTGGCCCTTTGGGGCCCTGGCATTTAGTCTCCGATGCCATTATTAGACA 247
 QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
 Db 248 AACTTGGAAACAGCTCTGGTAGAAGTGGGAGCCGGGTGAGCCAGAGCTGCATTACACC 307
 QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 Db 308 AAGGAGAACTGGGGAGGAGGCTGCATACCTCTCAGATGCTGATACAGACCACGC 367
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 Db 368 CAGGAGGAGAGAAACATCTCCACACCCGAAACACTTGGCCTCCACCTCCAGGAGCCCTC 427
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 Db 428 ACTGCCAGTAAAGTCCAAAGTATCACTCTATGGGAAGTCTGGGATTTGAAACAAATCTGC 487
 QY 161 TyrLysSerGlyValProLeuLeuGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
 Db 488 TACAAGTCAGAGATTCCTCCCTATTGAAATGGAATGATTGATGGATGATTTGAGAAGCTG 547
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
 Db 548 TTTCCGTCGTGATCTTACCCCTCGACTCTTCTGGAGGAGGAGCAAACTCCAAGG 607
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
 Db 608 GGCTCCGCTACCTGCCCGCCCGCCGGATATCCAGTGGACCAACCTGGATCCAGAGAG 667
 QY 221 LeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 Db 668 CTCTGAGAGAGCTGGGTCTCTTGGCTTCTGGGGCTTCCGGGAGCTGTAGACAAG 727
 QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
 Db 728 GCACAGTGGGCGCAGGCTTACGTGGGCGGCGCTGTCTGCACCTGTATGACCTCCATG 787
 QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
 Db 788 CCACCTAGTGGCCCGCCCAACCATCACAGAGGAGGCTCCCAATGTGGCTACAGAGCTGAGT 847
 QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
 Db 848 GGGGGTGTGCTGGCTTCTCCACAAATTCATGCACTGGCAGGAGGAATTTGCTGTGGGA 907
 QY 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
 Db 908 GGCAATGGCCAGAGACCCCGGAGAGCTGTGAGGGCAGAGGCGCTTCGAGAGACCTTC 967
 QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
 Db 968 TTGCTGATGAGTCCCGCCGAGCTGTACAGAGCATTTCCGGGGTGTACTATCAGACACATGAC 1027
 QY 341 IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
 Db 1028 ATTGGCTGGAGTGGAGGAGGAGCCAGCAGTGTCTACAAAGCTGGCAGCGGGCTTTGTG 1087
 QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
 Db 1088 CAGCTGGCCCGAGAGGAGGCTGCTGAGAACCGCTTCCAGAGAGATCCATGCTTCTCTCC 1147
 QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
 Db 1148 ACCACCTGGATAACATCTGTCGCTTCTCTGAAGTCAGTGTGCTGCTGCTGCTGCTG 1207

QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
 Db 1208 GGCATCTGCTCATGCTGGCTATGCTGTGTACCATGCTGGGTGGGACTGCGCCAG 1267
 QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
 Db 1268 TCCAGGTTCCGTGGGCTTCCGGGGTACTGCTGGTGGCCCTGGGGTGGCTCAGGC 1327
 QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
 Db 1328 CTTGGGCTCTGTCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCC 1387
 QY 461 PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu 480
 Db 1388 TTTTGGCTCTGGGAATCGGCGTGGATGAGTATTCCTGTGGCGCATGCCCTTCACAGAG 1447
 QY 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
 Db 1448 GCTCTGCTGGCACCTCTCCAGAGCGCATGGCGAGTGTCTGCAGCGCAGGGCACC 1507
 QY 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
 Db 1508 AGTGTGCTACTCATCATCATCAACATGCGCGCTTCCTCATGGTGGCTCGTTCCTCC 1567
 QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
 Db 1568 ATCCCTGGCTGGAGCTTCTCCTTACAGCC----- 1599
 QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
 Db 1600 -----ATCCTCAGCTGGACCTACCGCGCGCCACTGCCAG 1635
 QY 561 ArgLeuAspValLeuCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
 Db 1636 CGCCTTGATGTCTGCTCTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG 1695
 QY 581 ProGlnLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
 Db 1696 CCCAGAGCTGGGGAGCGGACAGTACCAGTGGGCAATGCCACCTCACTGCCACAGTT 1755
 QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
 Db 1756 CAAGCCTTATCCACCTGTGAAGCAGCAGCAGCATGTGTACCATCTCTGCCCTCCCAA 1815
 QY 621 AlaHisLeuValProProSerProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
 Db 1816 GCCACCTGTGTGCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTTCAGCCCTGGAGGG 1875
 QY 641 SerThrArgAspLeuLeuGlyGlnGluThrArgGlnLysAlaAlaCysLysSer 660
 Db 1876 TCCACAGGGACCTTCTAGGCCAGGAGGAGGAGCAGAGGAGGAGGAGGAGGAGGAGTCC 1935
 QY 661 LeuProCysAlaAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
 Db 1936 CTGCCCTGTGCCCTGGATCTTGCCAT-----TTCCGCCCGCGGAATTC 1980
 QY 681 LeuGln 682
 Db 1981 CTGCAG 1986
 RESULT 13
 AAT14220
 ID AAT14220 standard; cDNA; 5288 BP.
 XX
 AC AAT14220;
 XX
 DT 30-JUL-1996 (first entry)
 XX Human patched gene.
 DE
 XX Patched gene; ptc gene; embryo development; cellular regulation;
 KW signal transduction; ligand; antibody; hedgehog protein; gene therapy;
 KW ss.

XX OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 384..1427
 FT /*tag= a
 XX
 PN W09611260-A1.
 XX
 PD 18-APR-1996.
 XX
 PF 06-OCT-1995; 95WO-US013233.
 XX
 PR 07-OCT-1994; 94US-00319745.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Scott MP, Goodrich IV, Johnson RL;
 XX
 DR WPI; 1996-209842/21.
 DR P-PSDB; AAR75375.
 XX
 PT DNA encoding patched protein other than Drosophila patched protein - used
 PT to produce antibodies which detect or inhibit patched protein ligand
 PT signal transduction in cells.
 XX
 PS Example; Page 53-56; 70pp; English.
 XX
 CC A cDNA clone (AAT14220) coding for the human patched protein (PTC)
 CC (AAR75375) was obtd. by screening a human lung cDNA library with a 1 kb
 CC portion of the mouse ptc gene (see also AAT14218) and examination of
 CC isolated clones. The human ptc gene has about 89% identity to the mouse
 CC ptc gene. The 5' and 3' untranslated sequences are highly similar to
 CC mouse ptc, suggesting conservation of regulatory sequences. The human ptc
 CC gene can be used for prodn. of large amounts of recombinant PTC, as a
 CC probe e.g. to detect gene mutations in gene therapy, to study embryo
 CC development, to produce transgenic animal models, etc
 XX
 SQ Sequence 5288 BP; 1182 A; 1530 C; 1417 G; 1159 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 5,29e-245 Length: 5288
 Score: 3349.00 Matches: 662
 Percent Similarity: 70.02% Conservatives: 200
 Best Local Similarity: 53.78% Mismatches: 298
 Query Match: 53.40% Indels: 71
 DB: 2 Gaps: 16

US-09-990-046-2 (1-1203) x AAT14220 (1-5288)

QY 12 ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu--- 30
 Db 540 CCAGCTACTGC---GACGCGCGCTTCGCTCTGGAGCAGATTTCCAAGGGGAGGCTACT 596
 QY 31 -----LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
 Db 597 GCGCGGAAAGCGCCACTGTGGCTGAGAGCGGAGTTTCAGAGACTCTATTATAACTGGGT 656
 QY 49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuAlaPheGlyAla 68
 Db 657 TGTATATTCAAAAACCTCGCGCAAGTTCCTTGGTTGGGCTCTCATATTGGGGCC 716
 QY 69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
 Db 717 TTCGCGTGGGATTAAAGACGACGCAACCTCGAGACCACCGTGGAGGAGCTGTGGGTGGAA 776
 QY 89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGlnLysLeuGlyGluAla 108
 Db 777 GTTGAGGACGAGTAAGTCTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 836
 QY 109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGlnGluGlnLeuThr 128
 Db 837 ATGTTTAACTCTCACTCATGATACAGCCCTAAAGAGAGAGGTGCTAATGTCTTGACC 896

QY 129 ProGluAlaLeuGlyLeuHisLeuGlnAlaLeuThrAlaSerLysValGlnValSer 148
Db 897 ACGAAGCGCTCTTACAAACCTCGACTCGGCATCCAGGCCAGCCGCTCCATGTATAC 956
QY 149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db 957 ATGTACAACAGGCGAGTGGAAATTGGACATTGTGGTTACAAATCAGAGAGCTTATCACA 1016
QY 169 GluAsnMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuThrPro 188
Db 1017 GAAACAGGTTACATGGATCAGATAAGATAATCTTACCTTGTGGTTATATTACACCT 1076
QY 189 LeuAspCysPheTrpGluGlyAlaLeuLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
Db 1077 TTGACTGCTTCTGGGAAGGGCGAAATACAGTCTGGGACAGCATACCTCTTAGGTAAA 1136
QY 209 ProAspIleGlnTrpAsnLeuAspProGluGlnLeuLeuGluLeuGlyProPhe 228
Db 1137 CCTCCTTGGGTGGACAACTTCGACCTTTGGAAATCTCGGAAGATTAAAGAAATA 1196
QY 229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlnAlaTyr 247
Db 1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGCTGAGGTGTGTCATGGTTAC 1256
QY 248 ValGlyArgProCysLeuHisProAspLeuHisCysProProSerAlaProAsnHis 267
Db 1257 ATGACCGCCCTGCTCAATCCGGCGATCCAGACTGCCCGCCGACAGACCCCAACAAA 1316
QY 268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db 1317 AATTCAACCAACCTCTTGATATGGCCCTGTGTTGAATGGTGGATGTCATGGCTTATCC 1376
QY 288 HisLysPheMetHisTrpGlnGluGluLeuLeuGlyGlyMetAlaArgAspProGln 307
Db 1377 AGAAAGTATATGCACTGGCAGGAGGATGATTTGGTGGTGCGCACAGTCAAGAACAGCACT 1436
QY 308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db 1437 GGAACCTGCTAGCGCCATGCTCCAGACCATGTTCCAGTTAATGATCCCAAGCAA 1496
QY 328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db 1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC--ATCAACTGGAACGAGGAC 1553
QY 347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgPheValGlnLeuAlaGlnGluAla 366
Db 1554 AAGCGCGACGACCTCCCTGGAGGCTGCGCAGGACATATGTGGAGTGGTTCATCAGAGT 1613
QY 367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db 1614 GTGCGACAGACTCCACTCAAAAGTGTCTTCTTCCACACGACCCCTGGAGCATC 1673
QY 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db 1674 CTGAAATCCCTCTCTGACGTGAGTGTATCGCGTGGCCAGCGGTACTTACTCATGCTC 1733
QY 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db 1734 GCCTATGCTCTTAACCATGCTGCGTGGAGTGTCTTCCCAAGTCCCAGGGTGGCGTGGG 1793
QY 427 LeuAlaGlyValLeuLeuValAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCTGCTGGTTGACTGTAGTGGCTGCGAGACTGGGCCCTGTGCTCATTTG 1853
QY 447 LeuGlyIleThrPheAsnAlaAlaThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db 1854 ATCGGAATTCCTTAACTGCTGCAACACTCAGGTTTTTGGCAATTTCTCGCTCTTGGTGT 1913
QY 467 GlyValAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly----- 484
Db 1914 GGTGTGGATGATGTTTTTCTTCTGGCCCGCCCTTCAGTGAACACAGACAGATAAAGA 1973

QY 485 ThrProLeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTTCAGGACAGGACCGGGAGTGTCTGAAGCGCAGGACGCGTGGCCCTC 2033
QY 505 ThrSerIleAsnAsnMetalAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACGTCCATCAGCAATGTTCACAGCCTTCTTCATGGCCGCGTAAATCCCAATTCGCGCTG 2093
QY 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGCGGTTCCTCCAGGAGCGGTAGTAGTGTTCATTAATTTTGCATGGTTCTGCTC 2153
QY 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTCTCCTCAATTTTCAGCATGGATTATATCGCGGAGGACAGGAGCTGGATTT 2213
QY 565 LeuCysCysPheSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTTTACAAGCCCTCGTCAGCAGCAGTGAATTCAGGTGAACCTCAGGCCATC 2273
QY 585 GlyAsp-----GlyThrValProValGlyIleAlaHis----- 595
Db 2274 ACCGACACACACAGCAATACCCGCTACAGCCGCCCTCCCTACAGCAGCCACAGCTTT 2333
QY 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAACGAGATTTACCATCGAGTCCACGTCCAGCTCCGCGAGGAGTACAGCCC 2393
QY 609 SerSerGlnHisValThrIleLeuProProGlnAlaHisLeuValProPro--- 627
Db 2394 CACAGCAGCTGTACTACACCCGCTGAGCCGCTCCGAGATCTCTGTGCGAGCCGCTC 2453
QY 628 -----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGCAGCACCTTCAGCTGCCAGAGCCGAGAGACCACTCCACAAAGGAC 2513
QY 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTTCCAGTTCTCCGACTCC-----AGCTCCACTGCTCGAGCCCTCTGTACG 2567
QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2568 AAGTGGACACTCTCATCTTTTGTGAGAAGCACTATGCTCTTCTTCTTGAACCAAAA 2627
QY 685 AlaIysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGTGTATCTCTTTTCTGGGCTTCTGGGGTTCAGCTTTATGGCACC 2687
QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGACGGGCTGGACCTTACGACATTTGTACTCGGNAACACAGAGATAT 2747
QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCAAAATTCAAATACTTTCTTCTACAACATGTATATAGTCACCCAG 2807
QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAGACA---GACTACCCGAATATCCAGCACTTACTTTACGACCTACACAGGAGTTTCAGT 2864
QY 765 SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AAGCTGAGTATGTCATGTGGAGAAACAAACAGCTTCCCAAAATGTGGCTGCATC 2924
QY 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTTCAGGAGCTTCAGGATGCAATTTGACAGTCACTGGGAAACCGGAAA 2984
QY 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaValLysLeuLeu 824
Db 2985 ATCATGCCAAACAATATACAGAAATGATCAGATGGAGTCTTCTGCTCAACACTCCTG 3044
QY 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844


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Db      3045  GTCCAAACCGCGACCGCCGATAGCCCATGACATCAGCCAGTTCATTAACACGCGTCTG 3104
QY      845  ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrrpVal 864
Db      3105  GTGGATGCAGATGCATTAATATCCCGAGCGCTTCTACATCTACCTACCTGACGGCTGGGTC 3164
QY      865  SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu 884
Db      3165  AGCAACGACCGCGTGGTGTATGCTGCTCCAGGCCAACATCCGGCCACACCGACACAGAA 3224
QY      885  TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
Db      3225  TGGGTCCACGACAAAGCGCATACATGCTGAAACAGGCTGAGATCCCGGACGACAG 3284
QY      904  ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db      3285  CCCATCGAGTATGCCAGTTCCTCTTCTACCTCAACGGGTGGGGACACCTCAGACTTT 3344
QY      924  ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db      3345  GTGGAGGCAATTGAAAAGTAAGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTGTC 3404
QY      944  AlaTyrProSerGlySerProPheLeuPheTrrpGlnTyrLeuGlyLeuArgArgCys 963
Db      3405  AGTTACCCCAACGCTACCCCTTCTCTCTGGAGCAGTACATCGGCTCCGCCACTGG 3464
QY      964  PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db      3465  CTGCTGCTGTTCATCAGCGTGTGTGGCTTCGACATTCCTCGTGGCTGTCTTCCTT 3524
QY      984  LeuAsnProTrrpThrAlaGlyLeuIleValLeuValLeuAlaMetThrValGluLeu 1003
Db      3525  CTGAACCCCTGGACGCGCGGATCATGTGATGCTCTGGCGTGATGACGGTGGAGCTG 3584
QY      1004  PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValIleLeuVal 1023
Db      3585  TTCGGCATGATGGCCCTCATCGGAATCAGCTCAGTGGCGCGCTGGTTCATCTCTGATC 3644
QY      1024  AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db      3645  GCTTCTGTGGCATAGGATGGAGTTCACCGTTTCAGCTTGTGGCTTTCAGCGGCC 3704
QY      1044  GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db      3705  ATCGGCGACAAAGAACCGCGGTGTGCTGTCCTGGAGCACATGTTGCACCCGCTGCTG 3764
QY      1064  AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
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QY      1084  IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuHisGly 1103
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QY      1104  LeuValLeuLeuProValLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
Db      3885  CTGGTITTCCTCCCGTCTTGTCTTCTTGGACCATATCTCAGGTGTCTCAGCC 3944
QY      1123  tTyrLys-----GluSerProGluIleLeuSerProProAlaProGlnGlyG1 1139
Db      3945  AACGGCTTGAACCGCTGCGCCACACCTCCCTGAGCCACCCCGCCAGCG----- 3993
QY      1139  yGlyLeuArgTrrpGlyAlaSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db      3994  -----TGTTCGCGTTCGCGATGCGCGCG-----GCCAC 4022
QY      1159  rMetThrValAlaIleHisProPro----- 1167
Db      4023  ACCGACGCGGTCTGATTCCTCCGACTCGGAGTATAGTTCGACGACGAGTGTGAGGC 4082
QY      1168  -----ProLeuProGlyAlaTyrIleHisProAlaProAspG1 1180

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Db      4083  CTGAGCGAGGAGCTTCGGCTACTAGGAGCCAGCGGCGGGAGGCGCTGCCCCACAA 4142
QY      1180  uProProTrrpSerProAlaAlaThrSerSer 1190
Db      4143  GTGATCGTGGAGCCACAGAAAACCCCGTCT 4173

RESULT 14
AAV64093
ID   AAV64093 standard; cDNA; 5288 BP.
XX   AAV64093;
AC   AAV64093;
DT   26-JAN-1999 (first entry)
XX   Human patched gene.
DE   Human; patched gene; diagnosis; treatment; developmental disorder;
KW   cancer; healing; injured tissue; ptc; spina bifida; Wnt-1 oncogene;
KW   sperm production; gene therapy; ss.
XX   Homo sapiens.
OS   Homo sapiens.
FH   Key Location/Qualifiers
FT   CDS 384..4727
FT     /*tag= a
XX   US5837538-A.
XX   17-NOV-1998.
XX   06-OCT-1995; 95US-00540406.
XX   07-OCT-1994; 94US-00319745.
XX   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX   Scott MP, Goodrich LV, Johnson RL;
DR   WPI; 1999-023461/02.
DR   P-PSDB; AAW72969.
XX   Nucleic acid encoding vertebrate patched protein and related
XX   transformants - used to express poly:peptide(s), useful for diagnosis and
XX   treatment of developmental disorders or cancer, and in healing of injured
XX   tissue.
XX   Claim 1; Col 59-64; 38pp; English.
XX   The present sequence represents the human patched (ptc) gene. Cells
XX   containing and expressing the ptc gene are used for the recombinant
XX   production of the protein. These in turn are useful: (i) for generating
XX   antibodies (Ab); and (ii) to screen for specific-binding ligands
XX   (potential therapeutic agonists and antagonists). The ptc gene, or its
XX   fragments, are used to isolate related sequences from other mammals; to
XX   identify mutations (particularly those associated with genetic diseases
XX   such as spina bifida and other developmental disorders); to monitor
XX   expression levels in testis (to determine relationship with sperm
XX   production) and to isolate 5'-non-coding sequences (used to study
XX   embryonic development and to provide regulated expression of proteins).
XX   The complete gene can be used in gene therapy, including expression of
XX   antisense molecules, and to generate transgenic animals for studies of
XX   embryonic development. Ab are used diagnostically to determine the ptc
XX   protein on cell surfaces and as competitive inhibitors of signal
XX   transduction through the ptc ligand. Cells that have been engineered to
XX   express the ptc protein can be used to promote regrowth and healing of
XX   damaged tissue (e.g. growth of new teeth) and regulation of the ptc
XX   protein expression may be useful in cancer treatment (it may control the
XX   Wnt-1 oncogene)
SQ   Sequence 5288 BP; 1182 A; 1530 C; 1417 G; 1159 T; 0 U; 0 Other;
Alignment Scores: 5.29e-245 Length: 5288
Pred. NO.:

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Db	2568	AAGTGGACACTCTCACTTTTGGCTGGAGAGCACTATGCTCTTTCTCTTGGAAACCAAAA	2627
QY	685	AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla	704
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QY	705	ThrLeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHis	724
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QY	725	AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln	744
Db	2748	GACTTATGTGTGACAAATCAAACTACTTTCTTCTACACATGTATATAGTCACCCAG	2807
QY	745	GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer	764
Db	2808	AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACCTTACACGAGTTTCAGT	2864
QY	765	SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr	784
Db	2865	AACGTGAAGTAGTGTATGTTGGAAAGAAAAACAAACAGCTTCCAAAAATGTGGCTGCAC	2924
QY	785	TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg	804
Db	2925	TTCCAGAGCTGGCTTCAGGGACTTCAGATGCATTTGACAGTGACTGGGAAACGGGAAA	2984
QY	805	IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu	824
Db	2985	ATCATGCCAAACAAATTACAGAAATGGATCAGACATCGAGTCTTGGCTTCAAACTCTCG	3044
QY	825	IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu	844
Db	3045	GTGCAAAACCGGCAGCCGCGATAGACCCATCGACATCAGCCAGTTGACTTAAACAGCGCTG	3104
QY	845	ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal	864
Db	3105	GTGATGCAATGGCATCAITTAATCCAGCGCTTTCTACATCTACCTGACGGCTTGGGTC	3164
QY	865	SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu	884
Db	3165	AGCAACGACCCGTCGGGTATGTGCTCTCCAGGCCAACATCGGGCCACACCGACAGAA	3224
QY	885	TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln	903
Db	3225	TGGGTCCACACAAAGCCGACTACATCGCTGAAACAAAGCGTGAGATCCGGCAGCAGAG	3284
QY	904	ProLeuGlyPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe	923
Db	3285	CCCATCAGATGCCCCAGTTCCCTTTCTACTCAACGGGTGGGGACACCTCAGACTTT	3344
QY	924	ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis	943
Db	3345	GTGGAGCAATTGAAAAAGTAAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGCTCC	3404
QY	944	AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys	963
Db	3405	AGTTATCCCAACCGCTACCCCTTCCCTCTCTGGGAGCAGTGACATCGGCTCCGCCACTGG	3464
QY	964	PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu	983
Db	3465	CTGCTGCTGTTCATCAGCGTGGTGTGGGCTGCACATTCCTCGTGTGCGCTGTCTTCCTT	3524
QY	984	LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu	1003
Db	3525	CTGAACCCCTGGACGCCGGGATCATTTGTATGGTCTCTGGCGCTGAAGCGGTTCGAGCTG	3584
QY	1004	PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal	1023
Db	3585	TTCCGATGATGGCGCTCATCGGAATCAAGCTCAGTGTGCGCTGCTGTCATCTCTGATC	3644
QY	1024	AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr	1043
Db	3645	GCCTCTGTGGCATAGAGTGGAGTTACCGTTCAGTTGCTTTGGCCCTTCTGACGGCC	3704

QY	1044	GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr	1063
Db	3705	ATCGCGCAAGAAGACCGCAGGGCTGTGCTTCCCTGGAGCACATGTTTGACCCGTCCTG	3764
QY	1064	AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe	1093
Db	3765	GATGCGCGGCTGCATCTGCTCGGAGTGTGATGCTGGCGGATCTGAGTTTCGACTTC	3824
QY	1084	IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly	1103
Db	3825	ATTGTCAGGTATTCTTTGCTGCTGGCGATCTCTACCATCTCTCGCGGTCTCAATGGG	3884
QY	1104	LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal-IleGlnMe	1123
Db	3885	CTGGTTTGTCTCCCGTCTTTTCTCTTTCTTTGGACCATATCTGAGGTGTCTCCAGCC	3944
QY	1123	tTyrLys-----GluSerProGluIleLeuSerProProAlaProGlnGlyG1	1139
Db	3945	AACGGCTTGAAACCGCTGCCACACCTCTCCCTGAGCCACCCCCACGC	3993
QY	1139	yGlyLeuArgTyrGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrse	1159
Db	3994	-----TGTTCCGCTTCGCATGCCCCCG-----GCCAC	4022
QY	1159	rMetThrValAlaIleHisProPro-----	1167
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QY	1168	-----ProLeuProGlyAlaTyrIleHisProAlaProAspG1	1180
Db	4083	CTCAGCAGAGACTTCGGCACTACGAGGCCACGAGGCGCGGAGGCCCTGGCCACCAA	4142
QY	1180	uProProTyrSerProAlaAlaThrSerSer	1190
Db	4143	GTGATCGTGGAAAGCCACAGAAAACCCCGTCT	4173
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AAF32185	ID	AAF32185 standard; DNA; 5288 BP.	
XX	AC	AAF32185;	
XX	DT	12-APR-2001 (first entry)	
XX	DE	Human patched gene.	
XX	KW	Human; patched; PTC; segment polarity; limb patterning; development;	
XX	KW	hedgehog; antibody; mouse; ds.	
XX	OS	Homo sapiens.	
XX	FN	US6172200-B1.	
XX	PD	09-JAN-2001.	
XX	PF	20-OCT-1997; 97US-00954668.	
XX	PR	07-OCT-1994; 94US-00319745.	
XX	PR	06-OCT-1995; 95US-00540406.	
XX	PA	(STRD) UNIV LELAND S STANFORD.	
XX	PI	Scott MP, Goodrich LV, Johnson RL;	
XX	DR	WPI; 2001-136884/14.	
XX	DR	P-PSDB; AAB67163.	
XX	PT	Novel monoclonal antibody useful in diagnostic assays for detection of	
XX	PT	presence of protein on surface of cells specifically binds to naturally	
XX	PT	occurring patched protein, other than Drosophila patched protein.	
XX	PS	Disclosure: Col 57-62; 1990; English	

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Qy	387	LeuHicAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu	406
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Qy	505	ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu	524
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Qy	525	ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu	544
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Db	2154	ATTTTTCCTGCATTTCTCAGCATGGATTTATATCGAGCGGACGACGACCTGGATATT	2213

	Qy	565	LeucCysSerProCysSerAlaGlnValleGlnIleLeuProGlnGluLeu	584
		566:::.....:::.....:::	
	Db	2214	TTCGTGGTTTACAGCCCTCGTCAGCAGAGTGATTCAAGTGAACCTCAGGCCTAC	2273
		:::.....:::.....:::	
	Qy	585	GlyAsp-----GlyThrValProValGlyIleAlaHis-----	595
		586:::.....:::.....:::	
	Db	2274	ACCGACACACAGNCANTACCGCTACAGCCCCCACCTCCCTACAGCAGCCACAGCTTT	2333

Qy 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAAAGCGAGATTACCATGCAGTCCCACTGCCAGTCCCGACGGAGTACGAGCCC 2393

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 07:57:40 ; Search time 327 Seconds
(without alignments)
1302.800 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 10% summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3348	53.4	1447	8	US-08-954-701A-19
5	3348	53.4	1447	9	US-09-898-533-5
6	3348	53.4	1447	10	US-09-754-032-19
7	3348	53.4	1447	14	US-10-421-446-19
8	3337	53.2	1434	14	US-08-954-701A-10
9	3337	53.2	1434	10	US-09-754-032-10
10	3337	53.2	1434	14	US-10-421-446-10
11	3048	48.6	1296	14	US-10-302-279-60
12	2235	35.6	1311	8	US-08-954-701A-4
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14	2235	35.6	1311	14	US-10-421-446-4	Sequence 4, Appli
15	1992	31.8	1286	9	US-09-898-533-3	Sequence 3, Appli
16	1961.5	31.3	1299	8	US-08-954-771-48	Sequence 48, Appl
17	1961.5	31.3	1299	17	US-10-647-654-48	Sequence 48, Appl
18	1936.5	30.9	1285	8	US-08-954-701A-6	Sequence 6, Appli
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21	1708.5	27.2	1405	14	US-10-369-493-5464	Sequence 5464, Ap
22	992	15.8	714	14	US-10-369-493-5410	Sequence 5410, Ap
23	640	10.2	1278	14	US-10-208-731-2	Sequence 2, Appli
24	640	10.2	1278	14	US-10-741-601-530	Sequence 530, App
25	602.5	9.6	1319	14	US-10-208-731-4	Sequence 4, Appli
26	600.5	9.6	1359	15	US-10-621-758A-44	Sequence 44, Appl
27	600.5	9.6	1359	16	US-10-663-208A-44	Sequence 44, Appl
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40	557.5	8.9	1333	16	US-10-663-208A-12	Sequence 12, Appl
41	557.5	8.9	1333	16	US-10-646-301A-12	Sequence 12, Appl
42	557.5	8.9	1333	16	US-10-736-769-12	Sequence 12, Appl
43	444	7.1	933	15	US-10-415-934-3	Sequence 3, Appli
44	434	6.9	1061	15	US-10-415-934-9	Sequence 9, Appli
45	413.5	6.6	954	14	US-10-060-756A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-990-046-2
; Sequence 2, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990, 046
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-046-2

Query Match 100.0%; Score 6272; DB 9; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTRSPPLRLPPSYTPPARTAAQIILAGSLKAPLWLRAYFQGLLFSLGGCIQRHCKVLF	60
Db	1	MTRSPPLRLPPSYTPPARTAAQIILAGSLKAPLWLRAYFQGLLFSLGGCIQRHCKVLF	60
QY	61	LGLLAFGALGLRMAIITNLEQLVVEGVSQELHYTKELGEEAAYTSQMLIQATAR	120
Db	61	LGLLAFGALGLRMAIITNLEQLVVEGVSQELHYTKELGEEAAYTSQMLIQATAR	120
QY	121	QEGENILITPEALGLHLQAALTAKVQVSYLGKSWDLNKICYKSGVPLIENGMEIWKI	180
Db	121	QEGENILITPEALGLHLQAALTAKVQVSYLGKSWDLNKICYKSGVPLIENGMEIWKI	180


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QY 181 FPCVILTPDCFWEGAKLQGGSAVLPGRPDIQWNTLDPQELLBELGPPASLEGPRELLDK 240
Db 181 FPCVILTPDCFWEGAKLQGGSAVLPGRPDIQWNTLDPQELLBELGPPASLEGPRELLDK 240
QY 241 AQVQAVGVGRCPLHPPDLHCPSPAPNHHSRQAPNVAHELSCGGCHGFSHKFMHMQEELLG 300
Db 241 AQVQAVGVGRCPLHPPDLHCPSPAPNHHSRQAPNVAHELSCGGCHGFSHKFMHMQEELLG 300
QY 301 GMARDPOGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db 301 GMARDPOGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
QY 361 QLAQEALPENASQOIHAFTSTLDDILHAFSEVSAARVGVGYLLMLAYACVTMLRWDCAQ 420
Db 361 QLAQEALPENASQOIHAFTSTLDDILHAFSEVSAARVGVGYLLMLAYACVTMLRWDCAQ 420
QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFTE 480
Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFTE 480
QY 481 ALPGTPLQERMGECLQRTGTSTSVLTSSINNMAAFIIPALRAFSLQAAIIVVGCTFV 540
Db 481 ALPGTPLQERMGECLQRTGTSTSVLTSSINNMAAFIIPALRAFSLQAAIIVVGCTFV 540
QY 541 AVMLVFPAILSLDLRRRHQCORLDVLCFSPSCSAQVIQILPOELGDCGTVPGVIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRRHQCORLDVLCFSPSCSAQVIQILPOELGDCGTVPGVIAHLTATV 600
QY 601 QAETHCEASSQHVVTILPPQAHVLPSPDSPLGSELFSFGGSTRDLLGQEEETROKAAACKS 660
Db 601 QAETHCEASSQHVVTILPPQAHVLPSPDSPLGSELFSFGGSTRDLLGQEEETROKAAACKS 660
QY 661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db 661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG 720
QY 721 TKHAFLSAOLRVFSLVEVALVTOGGFDYAHSQBALFDLHORFSSLKAVLPPPAQAPRT 780
Db 721 TKHAFLSAOLRVFSLVEVALVTOGGFDYAHSQBALFDLHORFSSLKAVLPPPAQAPRT 780
QY 781 WLHYRNWLOGIQAAFPDQWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPDLSQLT 840
Db 781 WLHYRNWLOGIQAAFPDQWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPDLSQLT 840
QY 841 TRKLVDREGILPPELFWGLTVWVSSDPLGLAASQANFYPPPPWHLHDKYDTTGENLRIP 900
Db 841 TRKLVDREGILPPELFWGLTVWVSSDPLGLAASQANFYPPPPWHLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQPFLLRGLQKTADFVEATEGARAAACAEAGQGVHAYPSGSPFLFWEQYVGL 960
Db 901 PAQPLEFAQPFLLRGLQKTADFVEATEGARAAACAEAGQGVHAYPSGSPFLFWEQYVGL 960
QY 961 RRCFLLAVCILVCTFLVCALLLNPTAGILVILVAMMTVELFGIMFGFKLSAIPV 1020
Db 961 RRCFLLAVCILVCTFLVCALLLNPTAGILVILVAMMTVELFGIMFGFKLSAIPV 1020
QY 1021 ILVASVIGVGFTHVAGLFTTQGSNLRRAHALEHTFAPVTDGALSTLGLMLAGSH 1080
Db 1021 ILVASVIGVGFTHVAGLFTTQGSNLRRAHALEHTFAPVTDGALSTLGLMLAGSH 1080
QY 1081 PDFIVRVFFAALTVLTLGLHLGLVLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
Db 1081 PDFIVRVFFAALTVLTLGLHLGLVLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
QY 1141 LRWGASSLSPOSFARVTTMTVAIHPDPLPGAYIHPADDEPPWPSPATSSGNLSRSGFGP 1200
Db 1141 LRWGASSLSPOSFARVTTMTVAIHPDPLPGAYIHPADDEPPWPSPATSSGNLSRSGFGP 1200
QY 1201 ATG 1203
Db 1201 ATG 1203
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```
RESULT 2
US-09-909-280A-2
; Sequence 2, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THEREETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-280A-2

Query Match 99.6%; Score 6248; DB 9; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRSPPLRELPSPYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCQIQRHCGKVL 60
Db 1 MTRSPPLRELPSPYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCQIQRHCGKVL 60
QY 61 LGLLAFGALGALGRMAIETNLQWVEVGSRSVQELHYTKEKLGEEAAVTSQMLIOTAR 120
Db 61 LGLLAFGALGALGRMAIETNLQWVEVGSRSVQELHYTKEKLGEEAAVTSQMLIOTAR 120
QY 121 QEGENILTPALGHLQAALTASKVQVSLYKGSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENILTPALGHLQAALTASKVQVSLYKGSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDCFWEGAKLQGGSAVLPGRPDIQWNTLDPQELLBELGPPASLEGPRELLDK 240
Db 181 FPCVILTPDCFWEGAKLQGGSAVLPGRPDIQWNTLDPQELLBELGPPASLEGPRELLDK 240
QY 241 AQVQAVGVGRCPLHPPDLHCPSPAPNHHSRQAPNVAHELSCGGCHGFSHKFMHMQEELLG 300
Db 241 AQVQAVGVGRCPLHPPDLHCPSPAPNHHSRQAPNVAHELSCGGCHGFSHKFMHMQEELLG 300
QY 301 GMARDPOGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db 301 GMARDPOGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
QY 361 QLAQEALPENASQOIHAFTSTLDDILHAFSEVSAARVGVGYLLMLAYACVTMLRWDCAQ 420
Db 361 QLAQEALPENASQOIHAFTSTLDDILHAFSEVSAARVGVGYLLMLAYACVTMLRWDCAQ 420
QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFTE 480
Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFTE 480
QY 481 ALPGTPLQERMGECLQRTGTSTSVLTSSINNMAAFIIPALRAFSLQAAIIVVGCTFV 540
Db 481 ALPGTPLQERMGECLQRTGTSTSVLTSSINNMAAFIIPALRAFSLQAAIIVVGCTFV 540
QY 541 AVMLVFPAILSLDLRRRHQCORLDVLCFSPSCSAQVIQILPOELGDCGTVPGVIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRRHQCORLDVLCFSPSCSAQVIQILPOELGDCGTVPGVIAHLTATV 600
QY 601 QAETHCEASSQHVVTILPPQAHVLPSPDSPLGSELFSFGGSTRDLLGQEEETROKAAACKS 660
Db 601 QAETHCEASSQHVVTILPPQAHVLPSPDSPLGSELFSFGGSTRDLLGQEEETROKAAACKS 660
QY 661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG 720
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Db 661 LPCARWNLHAFARYQAPALLQSHAKAIVLVIFGALLGLSLYATLVQDGLATDVVPRG 720
Qy 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSLSKAVLPPPTAQAPT 780
Db 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSLSKAVLPPPTAQAPT 780
Qy 781 WLHYRNWLOGIQAAFDQDMSAGRIITRHSYRNGSDGALAYKLLIQTGDAQEPDLSOLT 840
Db 781 WLHYRNWLOGIQAAFDQDMSAGRIITRHSYRNGSDGALAYKLLIQTGDAQEPDLSOLT 840
Qy 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Qy 901 PAQPLEFAQFELRLGKQTDADFEAIEGABARAAAEAGQAGVHAYPSGSPFLFWEQYGL 960
Db 901 PAQPLEFAQFELRLGKQTDADFEAIEGABARAAAEAGQAGVHAYPSGSPFLFWEQYGL 960
Qy 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPV 1020
Db 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPV 1020
Qy 1021 ILVASGIGVEFTVHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
Db 1021 ILVASGIGVEFTVHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
Qy 1081 FDFIVRYFFAALT VLTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGG 1140
Db 1081 FDFIVRYFFAALT VLTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGG 1140
Qy 1141 LRWGASSLPPQSFAVTTMTVAIHPPPLPGAYIHPADPPPPSPAATSSGNLSSRGPG 1200
Db 1141 LRWGASSLPPQSFAVTTMTVAIHPPPLPGAYIHPADPPPPSPAATSSGNLSSRGPG 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 3
US-09-990-046-7
; Sequence 7, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: PI405R1
; CURRENT APPLICATION NUMBER: US/09/990, 046
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 7
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-990-046-7

Query Match 89.3%; Score 5599; DB 9; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

Qy 1 MTRSPPLRELPSPYTPPARTAPQIILAGSLKAPLWLRAYFQGLLPSLGGCIQRHCKVLF 60
Db 1 MTRPSLGEPLPSYTPPARTAPQIILAGSLKAPLWLRAYFQGLLPSLGGCIQRHCKVLF 60
Qy 61 LGLAFGALALGRMAIETNLEQLWVEGSRVQSQELHYTKELGEEAAYTSQMLIQTAH 120
Db 61 LGLVAFGALALGRVAIETDLEQLWVEGSRVQSQELHYTKELGEEAAYTSQMLIQTAH 120
Qy 121 QGENTILTPEALGLHLQAAALTASKVQVSLYSGKSWDLNKICYKSGVPLIENGMIERIEKL 180

Db 121 QGENTILTPEALGLHLQAAALTASKVQVSLYSGKSWDLNKICYKSGVPLIENGMIERIEKL 180
Qy 181 FPCVILTPDLCFWEKAGLQGSAYLPGRPDIQTWNLDPEQLLEELGPPFASLEGRELLDK 240
Db 181 FPCVILTPDLCFWEKAGLQGSAYLPGRPDIQTWNLDPEQLLEELGPPFASLEGRELLDK 240
Qy 241 AQVCQAVGRPCILHPDDLHCPSPAPNHHRSQAPNVAHELSCGGCHGFSKFMHWQBELLLG 300
Db 241 AQVCQAVGRPCILHPDDLHCPSPAPNHHRSQAPNVAHELSCGGCHGFSKFMHWQBELLLG 300
Qy 301 GMARDPOGELLARALALOSTFLMSPROLYEHFRGDYOTHDIGWSEEQASTVLQAWORRFV 360
Db 301 GTARDLQQLLRALALOSTFLMSPROLYEHFRGDYOTHDIGWSEEQASTVLQAWORRFV 360
Qy 361 QLAQALPENASQIHAFFSTTTLLDDIILHAFSEVSAARVWGGYLLMLAYACVTMLRWCAQ 420
Db 361 QLAQALPANASQIHAFFSTTTLLDDIILRAFSEVSTTRVGGYLLMLAYACVTMLRWCAQ 420
Qy 421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPPLALGIGVDDVFLLAHAFTE 480
Db 421 SQGAVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPPLALGIGVDDIIFLLAHAFTE 480
Qy 481 ALPGTLPQERMGECLORTGTSVVLTSINNMAAFILMAALVPIPALRAESLQAAIYVVGCTFV 540
Db 481 APDPTLPERMGECLRTSTGTSVALTSVNNVAFPMALVPIPALRAESLQAAIYVVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDCGTPVPGIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDCGTPVPGIAHLTATV 600
Qy 601 QATHCEASSQHVVTILPPOAHVPPPSDPLGSELSPSGSTRDLLQGESETRQKAAKCS 660
Db 601 QATHCEASSQHVVTILPPOAHVPPPSDPLGSELSPSGSTRDLLQGESETRQKAAKCS 660
Qy 661 LPCARWNLHAFARYQAPALLQSHAKAIVLVIFGALLGLSLYATLVQDGLATDVVPRG 720
Db 661 LCAHWTLAHAFARYQAPALLQSHAKAIVLVIFGALLGLSLYATLVQDGLATDVVPRG 720
Qy 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSLSKAVLPPPTAQAPT 780
Db 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSLSKAVLPPPTAQAPT 780
Qy 781 WLHYRNWLOGIQAAFDQDMSAGRIITRHSYRNGSDGALAYKLLIQTGDAQEPDLSOLT 840
Db 781 WLHYRNWLOGIQAAFDQDMSAGRIITRHSYRNGSDGALAYKLLIQTGDAQEPDLSOLT 840
Qy 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Qy 901 PAQPLEFAQFELRLGKQTDADFEAIEGABARAAAEAGQAGVHAYPSGSPFLFWEQYGL 960
Db 901 PAQPLEFAQFELRLGKQTDADFEAIEGABARAAAEAGQAGVHAYPSGSPFLFWEQYGL 960
Qy 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPV 1020
Db 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPV 1020
Qy 1021 ILVASGIGVEFTVHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
Db 1021 ILVASGIGVEFTVHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
Qy 1081 FDFIVRYFFAALT VLTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGG 1140
Db 1081 FDFIVRYFFAALT VLTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGG 1140
Qy 1141 LRWGASSLPPQSFAVTTMTVAIHPPPLPGAYIHPADPPPPSPAATSSGNLSSRGPG 1181
Db 1141 LRWDPRPTLPQSFAVTTMTVAIHPPPLPGAYIHPADPPPPSPAATSSGNLSSRGPG 1181

Sequence 19, Application US/08954701A
 Publication No. US20030032085A1
 GENERAL INFORMATION:
 APPLICANT: SCOTT, MATHEW P
 APPLICANT: GOODRICH, LISA V
 APPLICANT: JOHNSON, RONALD L
 TITLE OF INVENTION: Patched Genes and their Use
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley, Hoag & Eliot
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)
 CURRENT APPLICATION DATA:
 FILING DATE: 20-OCT-1997
 APPLICATION NUMBER: US/08/954,701A
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36709
 REFERENCE/DOCKET NUMBER: SUV-003.08
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1447 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-954-701A-19

Query Match 53.4%; Score 3348; DB 8; Length 1447;
 Best Local Similarity 49.9%; Pred. No. 9e-267;
 Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
 QY 12 PSYTPPARTAAPQILAGSL---KAPLMRAYFQGLLFLSLGCGIQHRCGKULFLGLAFGA 68
 DB 53 PSYC-DAFALEQISKGATGRKAPLWLRKAFQRLFLKLCYIQKNCCKFLVWGLLIFGA 111
 QY 69 LAIGLRMAITETMLEQLWVEGSRVSOELHYTKELGEEAAYTSQMLIQTARQGENILT 128
 DB 112 FAVGLKAANLETNVEELWVEGGRVSRRELNTYRQKIGEEAAYTSQMLIQTARQGENILT 171
 QY 129 PEALGLHQAALTASKQVSLYKGSWDINKICYKSGVPLIENGMIEMWIEKLFECVILTP 188
 DB 172 TEALLQHLDSALQASRVHYVYNNQWKLHLCYKSGELITETGYMDQIIIEVYECILITP 231
 QY 189 LDCFWEGAKQGGAYLPGRPDIQWNLDPQLLELGPFF-ASLEGFFELLDKQVQAYG 247
 DB 232 LDCFWEGAKLQSGTAYLLGKPLRWTFNFDPLFELELKKINYQVDSWEMLNKAIEVGHY 291
 QY 248 VGRPLETHDDLHCPSPANHHROAPNVAHELSCGHFSKFMHWQBEILLGGWARPDPQ 307
 DB 292 MDRECLFADPDPCATAPNKNSTKFLDVALVINGCGHLSKRYMEHQEELIVGGTVKNST 351
 QY 308 GELLAEALQSTFLIMSPPQYEHFRG-DYQTHPDIGNSEBOASTVQLQWQRFFVOLAQEA 366
 DB 352 GKLVSAHALQTMFQMLTPKQYEHFKGYEYVSH-INNEDKAAALIEAWQRTYVEVHQH 410
 QY 367 LPENASQOIHAFSPTLDDILHARSEVSAARVVGYYLIMLAYACVTMLRWDCAQSGSVG 426
 DB 411 VAQNSTQVLSTFTITLDDILKLSFSDSVIRVASGYLLMLAYACVTMLRWDCKSQQGAVG 470
 QY 427 LAGVLLVALVASGLGICALLGITPNAATTQVLPFLALGIGVDVDFILLAHAFTEALPG-- 484

DB 471 LAGVLLVALVASAGLGLCSLIGISFNAATTQVLPFLALGIGVDVDFILLAHAFSETQNK 530
 QY 485 TPLQRMGECLQRTGTSVLTSTNNVAAFLMAALVDIPALRAFSLOAAIVVGCTFVAVML 544
 DB 531 IPEDRTGECLRTGASVALTSISNVTAFMAALIPALRAFSLOAAIVVNFNFAVLL 590
 QY 545 VPAIILSLDRLRRHRCORLDVLCFSSPCSAQVQIQLPQELGD-----GTVPVGAH-- 595
 DB 591 IFFAILSMOLYRREDRLDIFCCFTSPCVSRVLOVEPQATYTHDNRYSFPFYSHSF 650
 QY 596 -----LATATQAFTHCEASSQHVVTIIPQAHLVPPP-----SDPLGSELFPGGSTRD 644
 DB 651 AHETQITMQSTVOLRTXDHPHTHYVTTAEPRSEISVQPVVTQDTLSCQSPSTSTRD 710
 QY 645 LLQGEETROKAAACKSLPCARWNLAHARYQFAPLLLOSHAKAIVLVFLGALLGLSLYGA 704
 DB 711 LLSQFSDS--SLHCLFPPCTKWTLSFAEKHYAPFLKPKAKVVVIFLFLGLLGLSVLYGT 768
 QY 705 TLVQDGLALTDVVPRTGKEHAPLSAOLRVPSLYEVALVTQGGFDYAHSQRALFDLHORFS 764
 DB 769 TRVRDGLDLTDIVPRETREVDYFAAQKFYSFYNNWIVTOKA-DYPNIQHLLYDHRFS 827
 QY 765 SLKAVLPPPATQAPRTWLYHYRNWLOGIQAAFQDQWASGRITRHSYRNGSEDEGALAYKLL 824
 DB 828 NVKYVMLEENKQLPKMWLHYFRDMLQGLQDAFDSMETGKIMPNYKNGSDDGVLAYKLL 887
 QY 825 IQGDAQEPFLDFSLQITRKLVDREGILPPELFYMGTLVWVSSDPLGLAAQANFYPPPE 884
 DB 888 VQTGSRDKPIDISQLTKQRLVDADGIIINPSAFYIYLTAWVSDNDFVAYAAQANIRPERPE 947
 QY 885 WLHDKYDTTGE-NLRIPPAQPLEPAQFPFLRLGRLOKQTADEVEATEGARAAACAQAGVH 943
 DB 948 WYHDKADYMPETRLRIPAEPIEYQAPFFYVNLGRLODTSDFEAELEKVRTICSNVTSGLS 1007
 QY 944 AYPGSGPFLFWEQYLGRLRCFLLAVALCLLVCTFLVOCALLLLNPTAGLIVLVLAMMTVEL 1003
 DB 1008 SYPNGYDFLFWEQYIGLRHWLLFISVLACTFLVCAVFLINPWTAGIIVWLALMTVEL 1067
 QY 1004 FGIMFLGKIKLSAIPVVLIVASVIGVEFTVHVALGELTTQGSNNRAAHAHLEHTAPVT 1063
 DB 1068 FGMMGLGKIKLSAVPVVILIASVIGVEFTVHVALAFLTAIGDKNNRAVLAHEMFAPVL 1127
 QY 1064 DGAISTLLGLLAGSHDFIVRYFFAALTATLTLGLLHGLVLLPVLISILGPPPEVI-- 1121
 DB 1128 DGAUSTLLGVMLAGSEDFIVRYFFAVLAILTLGLVNLGLVLLPVLISILGPPPEVSPA 1187
 QY 1122 ---QMYKESPE-----ILSP-----APOGG 1139
 DB 1188 NGLNRLTPSPPEPPSVVRFPAMPPTHGSGSDSDSEYSSQTTVSGLSGLSEELRHYEAQGA 1247
 QY 1140 G-----LRWG-----ASSSLFQSFAR 1155
 DB 1248 GPPAHQVIVEATENPVFAHSTVHVHPSRHHPPSNPROOPHLDSGLPPGROGQPRDPP 1307
 QY 1141 -----SMTVAIHPPLPGAYIHP 1176
 DB 1308 REGIWPPLYRPRRDAFELISTEGHSGPSNRARWGRGARSHNRPNPASTAMGSSVPGYQCP 1367
 QY 1156 VTT-----SMTVAIHPPLPGAYIHP 1176
 DB 1368 ITTVTASVTVAVHPPPPVPGFGRNP 1393

RESULT 5
 US-09-898-533-5
 ; Sequence 5, Application US/09898533
 ; Patent No. US20020106656A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gemmill, Robert M.
 ; APPLICANT: Drabkin, Harry A.
 ; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR,
 ; TITLE OF INVENTION: PATCHED

```

; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/898,533
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: US/09/268,140
; PRIOR FILING DATE: 2000-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-898-533-5

Query Match      53.4%; Score 3348; DB 9; Length 1447;
Best Local Similarity 49.9%; Pred. No. 9e-267;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAQAQILASGL---KAPLMRAYFOGLFLSLGCGIQHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAFALEQISKGKATGRKAPLWLRKAFQRLFLFKIGCYIQKNCCKFLVGVLLIFGA 111
QY 69 LALGLRMAITETNLEQLWVEGSRVSOELHYHTEKLGEEAAYTSOMLIQTARQGENILT 128
Db 112 FAVGLKAAITETNVEELWVEGSRVSELNVTYRQKIGEEAMPNQLMIQTPEEGANVLT 171
QY 129 PEALGLHQAALTAASKVQSVLYGKSWDLNCKYKSGVPLIENGMIENWIEKLRPCVILTP 188
Db 172 TEALLQHLDSALQASRVHVMYNEQWLEKLYKSGELITETGYMDQIIEVLYPCLLIITP 231
QY 189 LDCFWGAKLQGSAYLPGRPDITOWNLDPQLLEELGPF-ASLEGPRELLDKAQVQAY 247
Db 232 LDCFWGAKLQGSAYLPGRPDITOWNLDPQLLEELGPF-ASLEGPRELLDKAQVQAY 291
QY 248 VGRPCLHPDDLHCPPSAPNHSQAPNAVHELHSGCGHGFHCKPMHWOEELLGGMARDPQ 307
Db 292 MDRPCLNPADPCPATAPNKNSTKPLDMALVANGCGHGLSRKYMHWOEELIVGTVKNST 351
QY 308 GELLRAEALQSTFLMSPROLYBHFGRG-DYQTHDIGMSEBQASTVLQAWORRRFVOLAQEA 366
Db 352 GKLVSAHALQTMFLQMTFKQMYEHFGEYEVSH-INWNEKAAALIAEMWORTTVEVHHQS 410
QY 367 LPNASSQOIHAFSTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQSVG 426
Db 411 VAQNSTQKVLSTFTTTLLDILKFSFSDSVIRVASGYLLMLAYACVTMLRWDCAQSQSVG 470
QY 427 LAGVLLVALAVASGLGCLLGTENAAATQVLPFLALGIGVDVDFLLAHAFTEALPG-- 484
Db 471 LAGVLLVALAVASGLGCLLGTENAAATQVLPFLALGIGVDVDFLLAHAFTEALPG-- 530
QY 485 TPLQERMGECLORTGTSVVLTSINNMAAFLLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db 531 IFFEDRTGECLETGASVALTSISNTAFMAALIFIPALRAFSLQAAIVVGCTFVAVML 590
QY 545 VFPAILSLDIRRHORLORLVLCFSSPCSAQVITQILPOELGD-----GTVPVGIH-- 595
Db 591 IFFAILSMDLRYRDRRLDIFCCFTSPCVSRVITQVPEQAYTDHNTNRYSPPPYSSHSF 650
QY 596 -----LATVQAFTHCEASSOHVVTILPPQAHVPPP-----SDPLGSELSPGSGSTRD 644
Db 651 AHETQITMSTVQLRTEYDPHTHYVTTTAEPRSEISVQVPTVTQDTLSCQSPESSTRD 710
QY 645 LLGQBEETRQKACKSLPCARWNLHAFARYQAPILLOSHAKAIVLVFGALIGLSLYCA 704
Db 711 LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVVIIFLFLGLVGLSYLT 768
QY 705 TLVQDGLALTDVVPRTKEHAFSLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764
Db 769 TRVRDGLDLDIVPRETRYDEYFAAQKFVFSFYNMYIVTQKA-DYPNIQHLLYDLHRSFS 827
QY 765 SLKAVLPPATQAPRTLWLYHYNWLOGICQAAFDQWASGRITRHSYRNGSESGALAYKLL 824
Db 828 NVKYWLEENKQLPKMWCHYFRDWLQGLQDAFDSOWETGKIMPNNYKNGSDGGLVAYKLL 887

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QY 825 IOTGDAQEPLDFSQLTTRKLVDRGLIPPELFYMGLTIVWSSDPLGLAASQANFYPPPE 884
Db 888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHEPE 947
QY 885 WLHDKYDTTGE-NLRIPPAQPLEPAQPFLLRGKQKTADFVEATIEGARAACAEACQAGVH 943
Db 948 WYHDKADYMPETRLRIFAAEPIYAGFPFYJUNGURDTSDFVEAIEKVTIICSNYTSLSLS 1007
QY 944 AYPGSPFLFWEQYLGRLRCFLLAVCILLVCTFLVCALLLNPNWTAGLIVLVAMMTVEL 1003
Db 1008 SYNGPYFLFWEQYIGLRHMLLFIISVVLACTFLVCVAVFLNPNWTAGLIVLVAMMTVEL 1067
QY 1004 FGINGFILKLSAIPVIVLASVGIGVEFTVHVVALGELTTQGSRLNRAHALEHTFAPVT 1063
Db 1068 FGMGLIGIKLSAVPVVILLIASVGIGVEFTVHVVALGELTTQGSRLNRAHALEHTFAPVT 1127
QY 1064 DGAISTLLGLMLAGSHDFDIYRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVT-- 1121
Db 1128 DGAISTLLGLMLAGSHDFDIYRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVT-- 1187
QY 1122 ----QMYKESPE-----ILSPP-----APQGG 1139
Db 1188 NGLNRLTPSPPEPPSVVRFAFMPGHTHSGSDSDSEVSSQTTVYSGLSEELRHYEAQGA 1247
QY 1140 G-----LRWG-----ASSSLPQSFA 1155
Db 1248 GGAHQAIVTEATNPVFAHSTVHVHPSRHHPPNPROQPHLDGSLPPGQGGQPPRRDPP 1307
QY 1141 -----LRWG-----ASSSLPQSFA 1155
Db 1308 REGIWMPLYPRRDAFEISTEGHSGSNRARNRMPGRGARSHNPNRNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITTWTASVTVVAHVPPPPVPGGRNP 1393

RESULT 6
US-09-754-032-19
; Sequence 19, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
;              GOODRICH, LISA V
;              JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249

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; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-754-032-19

Query Match 53.4%; Score 3348; DB 10; Length 1447;
Best Local Similarity 49.9%; Pred. No. 9e-267;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAQAQILAGSL---KAPLWRAFYFGLLPSLGGCGTORHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAPALEQISKGATGRKAPLWRAKAFQRLFLKLCYIQKNGKFLVGLLIFGA 111
QY 69 LAIGLRMAITETNLEQLWVEGVSQOELHYTKELGEEAAYTSQMLIQATAROGENILT 128
Db 112 FAVGLKAANLEITNVEELWVEGVSRELNTYTRQKIGEEANFQPLMIQTPKEEGANVLT 171
QY 129 PEALGLHLAALTASKVQVSLYKGSWDLNKIKYKSGVPLIENGMIEMIEKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHVVMYKRWKLEHLCKYSGELITETGYMDQIIEVLYPCLITP 231
QY 189 LDCFWGAKLOGGSAYLPGRPDIQWNTMLDPEQLLELGPFF-ASLEGPRELLDKAUVQAY 247
Db 232 LDCFWGAKLOGGSAVYLLGKPLRWNTFDPLEFLEELKKNYQVDSWEEMLNKAEEVGHY 291
QY 248 VGRPCLPDLDHCPSPANHSQAPNAVELSGCHGFHKGPMHWOEEILLGGMARDPQ 307
Db 292 MDRPCLNPADPCPATAPNKNSTKPLDMALVNGCGHGLSKRYKMHWOEEILLVGGTVKNT 351
QY 308 GELLIRABALOSTFLMSPROLYEHFRG-DYQTHDIGMSEEQASTVLAQWQRRFVQLAQEA 366
Db 352 GKLVSAHALQTMQLMTPKQMYEHFKGYEVSH-INNEDKAAALEAMQRTYVVEVHQ 410
QY 367 LPENASQIHAFSSTLLDDILHAFSEVSAARVGGYLLMLAYACVWMLRWDCAOSQSGV 426
Db 411 VAQNSTQKLSFTTLLDDILKSPDSVSVIRVASGYLLMLAYACVWMLRWDCAOSQSGV 470
QY 427 LAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIVDDVDELLAHAFTEALPG-- 484
Db 471 LAGVLLVALSVAAGSLGICSLIGISFNAAATQVLPFLALGIVDDVDELLAHAFSTGQNR 530
QY 485 TPLQRMGECLQRTGTSVLTSLINMAAFMAALVPIPALRAFSLOAAIVVGCFTFVAVML 544
Db 531 IPPEDRTGECUKRTGASVALTSISNVTAFTFAALIPIPALRAFSLOAAIVVVFAMVLL 590
QY 545 VFPAILSLDURRHCRQLDVLCCFSSPCSAQVIQILFQELGD-----GVTPVGLAH-- 595
Db 591 IFFAILSMGLYRREDRLDIFCCFTSPCSRVIQVEPQAYTDTHTNTRYSPPPYSSHSF 650
QY 596 -----LTAIVQAFTHCEASSQHVVTLLPQAHVLEPP-----SDPLGSELFSFGSTRD 644
Db 651 AHETQITMQSTVQURTEYDPHTHYVYTTAEPRSEISQVPTVTDITSCQPESTSTRD 710
QY 645 LLGQEEETROKAAKSLPCARWNLAFARYQAFLLQSHAKAIVLVFLGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPECTKWTLSFPAEKHYAPFLPKAKVWVIFLFLGLGVSLEYGT 768
QY 705 TLVQDGLALTDPVPRGTEKHAFLSNOLRYFSLYVALVTCGGFYAHSORALFDLHQRES 764
Db 769 TRVRDGLDITDIPRETREYDFIAQAQFYKFSYNNYIVTQKA-DYPNIQHLLYDLHRSFS 827
QY 765 SLKALPPATQAPRTWLHYVRNWLQIQAQFDQDQWASGRITRHSYRNGSDGALAYKLL 824
Db 828 NVKYVLEENKQLPKWMLHYFRDMLQGLQDAFSDWETGKMPNNYKNGSDGGLVAYKLL 887
QY 825 IQTGDAQBPPLDPSQLTTRKLVDRGLIPPELFYMGLTWVWSDPLGLAASQANFYPPPPPE 884
Db 888 VQTGRDKPIDIQLTKQLKRLVDADGIINPFAFYIYLTAWVSNPDVAVYAAASQANIRPHRPE 947
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885 WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAAGAGVH 943
948 WVDKADYMPETRLRIPAAEPIEYQAQFPYLYNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007
944 AYPGSPFFLWEQYGLRRCFLLAVCILVCTFLVCALLLLNPWTAGLIVLVMVMTVEL 1003
1008 SYENGYPFLWEQYIGLRHLLIFISWLACTFLVCAVFLNPWTAGIIVMLALMTVEL 1067
1004 FGIMPLGLIKLSAIPVILVASGIGVEFTVHVALGFLTTQSGRNLRRAAHLEHTFAVT 1063
1068 FGMGLIGLIKLSAIPVILVASGIGVEFTVHVALGFLTTQSGRNLRRAAHLEHTFAVT 1127
1064 DGAISTLLGLLAGSHFPIVRYFFAALTVTLGLLHGLVLLPVLLSLILGPPPEVI-- 1121
1128 DGAIVTLLGLVLAGSEFDFIVRYFFAVLAILTILGLVGLVLLPVLLSPFGFVPEVSPA 1187
1122 ---QMYKESPE-----ILSP-----ADQGG 1139
1188 NGLNRLPTSPPEPPSVVRFAFMPGHTHSGSDSDSEYSSQTTVSGLSELRHYEAQGA 1247
1140 G-----LRWG-----ASSSLPQSFA 1155
1248 GGAHVQIVTEATNPVFAHSTVVPSSRHHPPNPRQQLDGSGLPPGQGGQPRDPP 1307
1141 ---LRWG-----ASSSLPQSFA 1155
1308 REGIMWPLYPRDAREISTEGHSGPSNRARWGRGARSHRNPRNPASTAMGSSVEGYCQP 1367
1156 VTT-----SMTVAIHPPPLDGAIVHP 1176
1368 ITTWTASVTVAVHPPPVPGGRNP 1393

RESULT 7
US-10-421-446-19
; Sequence 19, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
```

:	TELEFAX: 415-398-3249
:	INFORMATION FOR SEQ ID NO: 19:
:	SEQUENCE CHARACTERISTICS:
:	LENGTH: 1447 amino acids
:	TYPE: amino acid
:	STRANDEDNESS: single
:	TOPOLOGY: linear
:	MOLECULE TYPE: protein
:	SEQUENCE DESCRIPTION: SEQ ID NO: 19:
:	US-10-421-446-19
Query Match	53.4%; Score 3348; DB 14; Length 1447;
Best Local Similarity	49.9%; Pred. No. 9e-267;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;	
Qy	12 PSYTPPARTAAPQIIAGSL---KAPLMRLAYFOGLLFSLGCGIORHCGCKVLFLGLLAFGA 68
Dd	53 PSYC--DAFALEQISKGKATGRKAPLMRAKFQRLLFKLCGYIQKNGCKLVGLVLIIFGA 111
Qy	69 LALGRMAIETNLEQLWVEVGSRVSSELHYTKELGEAAAYTSQMILITAROEENILT 128
Dd	112 FAVGLKAANEETNYEELWEVGGRSRELNTROKIGEAMFNQPMIQTKEEGANVLIT 171
Qy	129 PEALGLHLQAALTASKVOVLSYGSKSDLNKI CVKSGVPLILENGMIENMWIEKLPCVILTP 188
Dd	172 TEALLQHLDNALQASRVHVVTMYNRQMKLEHCYKSGELITETGYMDQIIEYLXPCLTIPT 231
Qy	189 LDCEWEGAKLQGSAYLPGRPDIOQTNLDPQEELLEELGPF--ASLEGPRELLDKAUGVOAY 247
Dd	232 LDCEWEGAKLQSGTAYLLGPKPLRWTFDPLEFLEECLKINYQVDSWEEMLNKAEVGHGY 291
Qy	248 VGRPCLHPDDLHCPPSPAPNHSHSQAPNVAAHELGGCHGFHGKFMHWBOEILLGGMARDPQ 307
Dd	292 MDPRCLNPADPCDPATAPNKXSTKPLDMALVALNGGCHGLSRKTMHWBOEELLIVGTVKNST 351
Qy	308 GELLRAEALOSTTLLMSPROYLXEHRFG-DYQTHDIGWSEQASTVLCAWQRRVFOLAOEA 366
Dd	352 GKLVSAHALQTMQLMTPKQMEHFKEYEVSH-INNEDKAAAILAEAWORTYVEVVHQSS 410
Qy	367 LPENASQIHAFSSTLLDDILHAFFSEVASRVRVGVGYLLMLAYACTVMLRWDCAQSOGSVG 426
Dd	411 VAQNSTQKVLSFTTTLLDDILKSFSDSVSVIRVASGYLLMLAYACLFWLRWDCKSKSOAVG 470
Qy	427 LAGVILVALAVASGLGLCALLGHTFNNAATQVLPFIALGIGVDVDFLLAHAFTEALPG-- 484
Dd	471 LAGVILVALVSAAGLGLCSLIGISFNAATTQVLPFALGVGVDDVDFLLAHAFSETGNKR 530
Qy	485 TPLQRMGECLQRTGTSVWLITSNNMAAFUMLAALVIPALRAFSLQAAIVVGCTFFVAVML 544
Dd	531 IPEDRTGECIKXTGASVALTSISNVTAFPMALIIPALRAFSLQAAVVVFNFAMVLL 590
Qy	545 VPFAILLSDLRRRHCRQLDVLCSCFPSCAQVIQILPQELGD-----GTPVPVGI AH-- 595
Dd	591 IFFAILSMIDLXRREDRRLDIFCCFTSPCVSRVIVQEPQAYTQTHDNTRYSPPPPSSHFF 650
Qy	596 -----LTATVQAFTHCASSQHVUTLIPQAHLVPPP-----SDPLGSELFSPGSTRD 644
Dd	651 AHETQITMQSTVOLRTEYPDPTHVYVYTAEPRSEISVQPVTQDTLSCQSPESTSSTD 710
Qy	645 LLGQEEETRQKAACKSLPCARNLIAHFARYQFAPILLOSHAIAIVLVIFGALLGLSLYGA 704
Dd	711 LLISQFSDS--SLHCLPEPCKTTLSSFAEKHYAPFLKKPAKVWVIFLFLGLLGVSLYGT 768
Qy	705 TLVQDGLALTDVVPRGTKEHAFLSAQURYSFYSLYEVALVTQGGFDYAHSORALFDLHOREFS 764
Dd	769 TRVRDGLDLTDIVPRETRVEDVIFAQKFKYFSFNMYIVTQKA-DYPNIQHLYLDLHRSES 827
Qy	765 SLKAVLPPEATQAPRTWLHYRNWLQGIQAADFQDWASGRITRHSYRNGSEDGALAYKLL 824
Dd	828 NTKYVMLEENKQLPWMLHYFRDLWLOGLQDAFDSOWETGKIMPNNYKNKGSDDGVLAYKLL 887
Qy	825 IOTGDAQEPLDFSOLTTRKLVDREGILPPELFVMGLTWVWSDDPLGLAASQANFPFPPE 884

; TOPOLOGY: linear	
; MOLECULE TYPE: protein	
US-08-954-701A-10	
Query Match	
Best Local Similarity 53.1%; Score 3337; DB 8; Length 1434;	
Matches 672; Conservative 206; Mismatches 309; Indels 78; Gaps 20;	
QY	3 RSPPLREL--PPSYTPPARTAQAQIAGSL---KAPLWRAYPQGLLFSLGGCGIQHCKG 57
DB	28 RAAPDRDYLHRPSYC--DAAPALRQISGKATGRKAPLWLRRAKQRLFLKLCYIQKCGK 86
QY	58 VFLGLGALGALGALGRMAIETNLQWLVEGSRVSOELHYTKELGEEAAATYSQWLQ 117
DB	87 FLVVGLLIFGAFVAGLKAANLETNBELWVEGVRVSRLEINTRYQKIGEEAMFNPMQIMQ 146
QY	118 TARQEGENTILTPALGLHQAALTASKVQVSLYKSGWDLNKKICYKSGVPLIENGMIEMWI 177
DB	147 TPKEEGANVLITTEALLQHLDSALQASRVHYMYNRQWKLEHLCKYKSGELITETGYMDQII 206
QY	178 EKLFPVCLTPLPCFWEKAGLQGSAYLPORPDIQWNTLDPBQLBELGPF--ASLEGFRE 236
DB	207 EYLYPCLIITPLPCFWEKAGLQGSAYLPORPDIQWNTLDPBQLBELGPF--ASLEGFRE 266
QY	237 LLDKAQVQAYVGRPCLPDLDLHCPSPAPNHHSRQAPNVAHELSGGCHGFSHKFMHWOER 296
DB	267 MLNKAEGVGHGMDRPNADPCAPAPNKNSTKPLDVALVNGGCGQLSRKYMHWQEE 326
QY	297 LILGGMARDPQGBLLRAEALQSTFLMSPRQLYEHFRG--DYQTHDIGWSEEQASTVLQAW 355
DB	327 LIVGTVKNATKGLVSAHALQTMQTPKQMYEHFRGYVSH--INWNEDRAAAILLEAW 385
QY	356 QRRFVQLAQBALPENASQOIHAFSSSTLDDIHLAFSEVSAARVVGGLMLLAVACTMRL 415
DB	386 QRTYVEVHQSAPNSQKVLPTFTTTDLKSFSDSVIRVASGYLLMLAYACTMRL 445
QY	416 WDCAQSGVGLAGVLLVALAVASGLGALGTTENAAQTQVLPFLALGIGVDVDFLLA 475
DB	446 WDCSKSGVGLAGVLLVALAVASGLGALGTTENAAQTQVLPFLALGIGVDVDFLLA 505
QY	476 HAFTEALPG--TPLOERMGECLORTGTSVVLTSINNMAAFMLAALPIPALRAFSLQAAI 533
DB	506 HAFSETQNKRIPEDETGTGCKLTGASVALTSISNVTAFEMALIPALRAFSLQAAV 565
QY	534 VVGCTFVAVMLVPAIILSLDRRHCRQRLDLVLCFSPSCSAQVQIILPQBLG----- 586
DB	566 VVVFNFAMVLLIFPAILSMDLRYRDRRLDFCCFTSPCVSRVQVPEQAYTEPHSNTRY 625
QY	587 GTVPVGTAG-----LTATQAFTHCEASSQHVVTILPQOAHVPPP-----SDPLGS 633
DB	626 SPPTPYTSHFAHETHITMGTQVLRTEYDHTHYVYTTAEPRSEISVQPVTVTQDNLSC 685
QY	634 ELFSFGSTRDLQGBETRQKAAKSLPCARMNLAHFARYQFAPLQLQSHAKAIVLVLF 693
DB	686 QSPBSTSTRDLQGBETRQKAAKSLPCARMNLAHFARYQFAPLQLQSHAKAIVLVLF 743
QY	694 GALLGLSLYATLVQDGLATDVVPRGTKEHAFSAQLRFLSLEVALVITQGGDYAHSQ 753
DB	744 LGLLGVSLYGTTRVDRGLDLDIIVPRETREYDFTAQFKYFSFYNNYIVTQKA--DYPNIQ 802
QY	754 RALFDLHQRSSKLAVLPPAPATAPRTWHLHYRNWLGIOAAPPQDQWASGRITRHSYRNG 813
DB	803 HLLYDLHKSFSNVKVMLEENKQLPQWHLVFRWLQGLQDAFSDDETGRIMENNYKNG 862
QY	814 SEDGALAYKLIQTDGAQEPDLQFSLQTLTKLVDRGLIPPLFYNGLTVVWSSPFLGLAA 873
DB	863 SDDGVLYAKLVQTSRDKPIDISQTLKQRLVADADGIINPSAFYIYLTAWVSNDFVAYAA 922
QY	874 SQANFYPPPPWHLHDKYDTTGE--NLRTPPAQPLEFAQEPFLRLGLQKTADFEVELEGARA 932
DB	923 SQANIRPBPWHDKADYMPETRLRIPAAPEIEYAQFPFYNGLDRDTSDFVEALEKVRV 982
QY	933 ACABAGQAGVHAYPSGSPFLFWEQYIGLRRCLLAVCILLVCTFLVACALLLNPNWTAGLI 992

983 ICNNTYSLGSSVPEYNGYPLFWEQYISLRHLLLSISVVLACTFLVCAVELLNPNWTAGII 1042

993 VLVAMTVELFGIMGFLGKLSAIPWILVASVGIGVEFTVHVVALGELTTCQSRNLRAA 1052

1043 VNVALMTVELEFGMGLGKLSAIPWILVASVGIGVEFTVHVVALGELTTCQSRNLRAA 1102

1053 HALEHTFAPVTDCAISTLGLMLAGSHDFIVRYFFAALTIVTLGLGLHGLVLLPVLLS 1112

1103 LALEHMFAPVLDGAVSTLGLVMLAGSEDFIVRYFFAALTIVTLGLVNLGLVLLPVLLS 1162

1113 ILGPPPEVI-----QMYKESPEILSPP-----APQGGGLRMGASSSLPQSFAVTVTS-- 1159

1163 FFGCEPEVSPANGNLRLTPSPD--PPPSVVRFAVPPGHTNNGSDSSDSEYSSQTTVSGI 1220

1160 -----MTVAHPPPLPGAYTHP--APDDEPPSPAA---TSSGNLS 1194

1221 SEELROYEAQAGGAPAHQVIVEATENPVFARSTVVHPDSRHPPLTPRQQPHLDSGLS 1280

1195 SRPGP 1199

1281 ---PG 1282

RESULT 9

US-09-754-032-10

Sequence 10, Application US/09754032

Publication No. US20030148388A1

GENERAL INFORMATION:

APPLICANT: SCOTT, MATHEW P

GOODRICH, LISA V

JOHNSON, RONALD L

TITLE OF INVENTION: Patched Genes and their Use

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09754,032

FILING DATE: 03-Jan-2001

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/540,406

FILING DATE: 06-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: a60190-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1434 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-754-032-10

Query Match 53.2%; Score 3337; DB 10; Length 1434;
Best Local Similarity 53.1%; Pred. No. 7.2e-266;
Matches 672; Conservative 206; Mismatches 309; Indels 78; Gaps 20;

Db 28 RAAPDYLHRSYC--DAAFALQISKGKATKPKAPLMLRAKFORLLFLKGLCVIOKNCKG 86
QY 58 VFLGLLAFGALALGRLMAIETNLRLQWVSGRSVSOELHYHTEKLGEEAAYTSQMLIQ 117
Db 87 FLVGLLIIFGAFVGLKAANLETNVBEELWVEVGRVSRREINLYTRQIGBEAMFNPLMIQ 146
QY 118 TARQEGENILTPALGHLQAALTASKVQVSLYKSKMDLNKIKYKSGVPLIENGMEIEM 177
Db 147 TPKEGANVLTTTALLQHLSDASQAQRHVHYMTNRQWKLEHLCKSGELITETGYMDQII 206
QY 178 EKLFPVCVILTPDLFCWEGAKLOGGSAYLPGRPDIOQNTLNDPEQLLEELGPF-ASLEGPRE 236
Db 207 EYLYPCLIITPLDCFWEGAKLOGSTAYLLGKPLRWTNPDPLFLEELKKINQVDSWEE 266
QY 237 LLDKAQGVAYGVRPCLHPDDLHCPSPAPNHHGRQAPNVAHELSCGCHGSHKPMWQEE 296
Db 267 MLNKAIEVGHYMDRPPCLNPADPCPATAPNKNSTKPLDVALVNGGCGGLSRKYMWQEE 326
QY 297 LILGGWARDPQGLLRAEALQSTFLMSPROLYEHFERG-DYQTHDIGWSEQAQSTVLQAW 355
Db 327 LTVGGTVKNTGKLVSAHALQTFQMLTPKQMYEHFRGYDVSH-INWEDRAAAULEAW 385
QY 356 QRRFVOLAQBALPENASQQHAFSSTLDDILHAFSEVSAARVVGGYLLMLAYACVMTLR 415
Db 386 QRIYVEVHVQSVAPNSTQKVLPTFTTLLDILKSPSDSVIRVASGYLLMLAYACVMTLR 445
QY 416 WDCAQSGVGLAGVLLVALAVASGLGLCALLGITFNAATQVLPFLALGIGVDDVVELLA 475
Db 446 WDCSKSQVGLAGVLLVALSVAAGLGLSLIGISFNAATQVLPFLALGIGVDDVVELLA 505
QY 476 HATEALPG--TPOERMGECLORTGTSVVLTSINNMAFLMAALVIPALRAFSLQAAI 533
Db 506 HAFSETQCNKRIPEFTGTGLCKRTKGTASVALTSINVTAFMAALIPALRAFSLQAAV 565
QY 534 VVGCTFVAVMLVFPAILSLDRRRHQRDLVLCFCFSPCSAQVLIQILPQELGD----- 586
Db 566 VVNFNFAWVLLIPAILSMDLRYREDRLDIFCCFTSPCVSRVIOVEPQAYTEPHSNTRY 625
QY 587 GTVPVGIH-----LFAVQAFTHCEASSQHVVTILPQAHVPPP-----SDPLGS 633
Db 626 SPPTPYTSHSFAHETHITMOSTVQLRTYDPHTHYVYTAPRSEISVQPVVTQDNLSC 685
QY 634 ELSPGSGSTRDLQGBETKQACKSLPCARNLAHFAFYQAPLQLQSHAKAIVLVLF 693
Db 686 QSPBSTSTDLQLSQFSDS--SLHCLPPTCKWTLSFAEKHYAPFLKPKAKVVVILLF 743
QY 694 GALLGLSLYGATLVQDGLALTVDVPRGTKEHAFSLAQLRYSLEYVALVTQGGFDYAHSQ 753
Db 744 LGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNNVITOKA-DYPNIQ 802
QY 754 RALEDLHQRFSSLKAVLPPATQAPRTWLHYRNWLOGIQAAPQDQWASGEITHRSYRNG 813
Db 803 HLLYDLHKFSFNKVMLEENKQPLQWMLHYFRDWLQGLQDAPFSDMETGRIMPNNYKNG 862
QY 814 SEDCALAYKLIQTDGAQEPDLDFSLTRKLVDRGLPPLFMYGLTWVWSSDPLGLAA 873
Db 863 SDDGVLAYKLLVQIGSRDKPIDISQLTKQLRVADAGIINPFAFYLYLTAWVNDPVAIA 922
QY 874 SQANFYPPPEWLHDKYDTTGE-NLRIPPAQPLEFAFPFLRLGLOKQTDADVEAIEGARA 932
Db 923 SQANIRPHRPEWHDKADYMPETRLRIPAAEPYEAQPFYVINGLRIDTSDFEVAIEKVRV 982
QY 933 ACAGAGQVHAYPSGSPFLWEOYGLRRCFLAVCTILVCAALLLNPTWAGLI 992
Db 983 ICNNYTSIGLSSYPNGYPFLWEQYISLRHMLLSISVVLACTFLVCAVFLNPTWAGII 1042
QY 993 VLVLAMTVELFGIMGFLGKLSAIPVVLVASVIGVEFTVHVALGELTTQGSNRLFAA 1052
Db 1043 VNVLAMTVELFGIMGFLGKLSAIPVVLVASVIGVEFTVHVALAELTAGDKNHEAM 1102
QY 1053 HALEHTFAPVTDGAIISTLLGLMLAGSHDFIVRYFFAALTIVTLGLLHGLVLLPVLLS 1112
Db 1103 LALEHMFAPVLDGAVSTLLGLMLAGSEDFIVRYFFAVALTILVGLVINGLIVLLPVLLS 1162

QY 1113 ILGPPPEVI-----OMYKESPEILSP-----APOGGGLRWGASSSLFPQSFAVTVTS-- 1159
Db 1163 FPGPCPEVSPANGLNPLTPSP--PPPSVVRFAVPPGHTNNGSDSDSEYSSQTIVSGI 1220
QY 1160 -----MTVALHPPPLPGAYIHP-APDEPPWSPAA-----TSSGNLS 1194
Db 1221 SEELRQYEAQAGGAGHQAQVIVEATENPVFAKSTVVHPPDSRHPPLTPRQQPHLDGSL 1280
QY 1195 SRGPG 1199
Db 1281 ---PG 1282

RESULT 11

US-10-302-279-60
Sequence 60, Application US/10302279
Publication No. US20030171566A1

GENERAL INFORMATION:

APPLICANT: Dean, Michael Carlton
Hahn, Heidi Eve
Wicking, Carol

Christiansen, Jeffrey
Zaphiropoulos, Peter G.
Gallani, Mae R.
Shanley, Susan Mary
Chidambaram, Abirami
Vorechovsky, Igor

Holmberg-Lindstrom, Erika

TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10302,279

FILING DATE: 22-No. US20030171566A1-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/857,636

FILING DATE: 16-MAY-1997

APPLICATION NUMBER: US 60/017,906

FILING DATE: 17-MAY-1996

APPLICATION NUMBER: AU P00011

FILING DATE: 21-MAY-1996

APPLICATION NUMBER: AU P00363

FILING DATE: 07-JUN-1996

APPLICATION NUMBER: US 60/019,765

FILING DATE: 14-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hyman, Laurence J.

REGISTRATION NUMBER: 35, 551

REFERENCE/DOCKET NUMBER: 015280-278200US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 1296 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

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Db      898 NPWTAGIIVVULAMTVELFGMGLIGIKLSAVPVLLIASVGIGVEFTVHVVALAFLTAI   957
QY      1045 GSRNLRAHALEHTFAPVTGAI STLGLLMLAGSHFDIVRYFFAAALTVLTLLGLHGL    1104
Db      958 SDKNRRAVLALEHMFAPVDGA VSTLLGVLMAGSEDFDIVRFFAVLA LTTILGVNGL    1017
QY      1105 VLPVLLSILGPPEV----- 1120
Db      1018 VLLPVLSSFGPYPEVSPANGL NRLPTPGPPPSVVRFAMPPEGTHSGSDSDSEYSSQ   1077
QY      1121 -----IQMY-----KESPEI 1130
Db      1078 TTVYSLSEELRHVEAQCGAGPAHQVIVEATENPFVAHSVTVHPESRHHPPDNPKOOPHL 1137
QY      1131 LS---PPAPQG-----GGL-----RWG----- 1144
Db      1138 DSGSLPEGRCQQPRDRPRFKGLWPL YLRPRD AFEISTEGHGPSNRARWGPRGARSHN 1197
QY      1145 -----ASSSIPOSFARVTT----- SMTVAIHPPPLPGAYIHP 1176
Db      1198 PRNPTSTMGSSVFGYCQPITTVT ASVTVAVHPPVPVFGCRNP 1242

RESULT 12
US-08-954-701A-4
; Sequence 4, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-954-701A-4

Query Match          35.6%; Score 2235; DB 8; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.5e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;

QY      18 ARTAAPQILAGSL---KAPLMRAYFOGLLFSGCGIGQRHCGRKVLFGLIAFCALALGLR 74
Db      41 AALAL-SELEKKNIGGGRTSWIRAWLFOEFLTGCFCCGACGYLVFAVIAVSTRGVK 100

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1137 Q-----GGGLRWGASSSLPQSFARVTTTMT 1161
1122 KCSHPHPRXSSSSGGDKSRTSKSAPRCPASLTIT 1160
RESULT 13
US-09-754-032-4
; Sequence 4, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fiehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-754-032-4
Query Match 35.6%; Score 2235; DB 10; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.5e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;

75 MAIETNLQWVSGRSVQELHYTKELGEEAAYTSQMLIQARQEGENILTPALGL 134
101 SAQHTRVQWVQEGRLAEALKYTAQALGEADSTHQLVIQTAKDPDVSLLHPGALLE 160
135 HLOAALTASKVQVSLYKGSWDLNKIKYKSGVPLIEN-GMIEWMIKLPFCVILTPDLCFW 193
161 HLKVVHAATRVTHMYDIEMRLKDCYSPSIDPFGYHHIESIIDNVIPCAIITPDLCFW 220
194 EGAKLOGGS--AYLPG-RPDIQWNLDPDLEQLLEELG-----PFASLEGFRELDDKAQVG 244
221 EGSKLLGPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
245 QAYVGRPCLPDLDLHCPSPAPNHHRSQAPNVAHELGGCHGPHSKFMHWOEBELLGGMAR 304
278 SAYMKKPCLPDTPDPCPATAPNKKSGHIPDVAELSHGCGYFAAAYMHWPEQIIVGATR 337
305 DPQGEILRAEALQSTFLMSPROLYEHFRGDYOTHDIGWSEBOASTVLQAWQRRFVQLAQ 364
338 NTSALRKARXLQTVQVLMGEREMEWYADHYKVHQLGWNQEKAAAVLDWQKFAAEVR 397
365 EALPE---NASQIHFASSTLDDILHAFSEVAARVVGGLLMLAYACVTMLRW-DCAQ 420
398 KITTSVGSVSAYSFYPSTSLNDILGKFSEVSLKNILGYMEMLIYVAVTLQWRDPIR 457
421 SQSGVLGAVLLVALAVASGLGICALLGITFNAAATQVLPFLAIGIGVDVFPILAHAFTE 480
458 SQAGVGIAVLLLSITVAAGLGCALLGIPFNASTQIVPFLALGLGVQDMFLTHTHYVE 517
481 ALPGTLPQREWGECLOQTGFSVVLTSINNMAAFMAALVPIPALRAFSLQAAIVGVGTFV 540
518 QAGDVPREERTGLVKKSGSLVSLIASCNVMAFLAAALFIPAPFVCLQAAILLENLG 577
541 AVMLVFPAILSLDLRRRHRCORLDVLCF--SSPCSQAQVIQILPQELGDTVPVGVIAHLTA 598
578 SILLVFPAMISLDRRSARADLLCMLPESP-----LPKK---KIP-----617
599 TVQAFTHCEASSQHVITLIPQAHVLPDPPDPLGSELFPSCGGSTRDILGQEBEETRQAAAC 658
618 -----ERAKTRKNDKTHRTDTRQPLDPDV-----SENVTKTC 651
659 KSLPCARWNLAHFARYOFAPILLOSHAKAIVLVLFGLLGLSLYCATLVODGLATDPWP 718
652 LSVSLTKW-----AKNQYAPFIMPAVKVTSMLALIAVILTSWGAIKVKDGLDITVP 706
719 RGTKEHAFSLAQLRYFSLYEVALVTQGGFDYAHQSQRALFDLHORFSSLKAVLPPATQAP 778
707 ENTDEHEFLSQEKYFGFYNNMYAVTQGNFEYPTNQKLLYVHDQFVRIPNIKNNDGGLT 766
779 RTWLHYRNMLQGIQAAPDQDQWASGRITRHSY-RNGSEDEGALAYKLLIQTGDAEPDLFS 837
767 KFWLSLDFDWLLDQVAFDKEVASGCHITQEWCKNNSDEGLAYKLMVQTHVDNPIDKS 826
838 QLTT-RKLVDRREGILPPELFYMGTLTVWVSSDPLGLAASQANFYPPPELWLDHKYDITGEN 896
827 LITAGHLVDKGIINPAFNYLSANATNDALAYGASQGNLKPQQRWTHSPEDV---H 883
897 LRIPPAOFLEPAQFPFLGLRGKQKADFVEAIEGARAACAAGQAGVHAYPSGSPFLFWEQ 956
884 LEIKKSSPLIYQLPFVLSGLSDTSIKTLIRSVRDLCLKYEAKGLPNFPSPGIPFLFWEQ 943
957 YLGRRCPELLAVCILLVCTFLVCAILLINPWTAGLIVLVAMTVFELGINGELGKLSA 1016
944 YLYRLTSLLALACALAAVFAVMVLLLNAAVALVTLATLVQLLIGVWALLGVRLSA 1003
1017 IPVVILVASVGIGVEFVHVALGFLTTQGSNRLRAAHLEHTFAPVTDGAISTLLGLML 1076
1004 MPVULLVLAIGRVHFTVHLCIGFVTSIGCKERRASLALESVAPVHGAALAAASML 1063
1077 AGSHFDFTVRVFPFALTVTLILGLHGLVLLPVLLSILGPPPEVTOMYKESPEILSPAP 1136
1064 AASECGFVARLFLRLLLDIVELGLIDGLFFPILVLSILGPAEVRPI---EHPERLSTESP 1121

Db 278 SAYMKKPCLDPTDHPCHPATAPKKSCHTIPDVAELSHGCGYFAAAAYMEWPEQLIVGGATR 337
Qy 305 DPQGLLRAELQSTFLMSPROLYEHFRGDYQTHDIGHSEQASTVLOAWORFVQLAQ 364
Db 338 NSTSALRKARLQTVVQUMGERMEYKADHYKHQIOWNEKAADVADWQKFAAEVR 397
Qy 365 EALPE--NASQOIHAFSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRW-DCAQ 420
Db 398 KITTSALRKARLQTVVQUMGERMEYKADHYKHQIOWNEKAADVADWQKFAAEVR 457
Qy 421 SOGSVGLAGVLLVALAVASGLGCLCALGITTNAAQTQVLPALGIGVDDVFLLAHAFTE 480
Db 458 SOAGVGIAGVLLSITVAAGLGFACALLGIPNASTQIVPELALGLGVQDMFLTHITVE 517
Qy 481 ALPGTQERMECELOQTGTSVLTSTINNAAFMAALVPTPALRAFSLOAAIVVGCTFV 540
Db 518 QAGDVPRERTGLVKKSGSLVLAASCNVMAFLAAALLPAPRVFVCLQAAILLFLNLG 577
Qy 541 AVMLVFPAILSLDRRHRCORLDVLCF--SSPCSAQVIQLPOBLGDTGTPVGVIAHLTA 598
Db 578 SILLVFPAMISLDRRSARADLLCCLMPESP-----LPKK-----KIP----- 617
Qy 599 TVQAFTHCEASSQHVITLPPQAHVPPSPDPLSELFPSPGSTRDLGQEEETRKAAC 658
Db 618 -----ERAKTRKNDKTHRIDTTRQPLDPV-----SENVTKTC 651
Qy 659 KSLPCARWLAHAFARYOPAPILLQSHAKAIVLVLFGLLGLSLYGATLVQDGLALTDPVP 718
Db 652 LSVSLTKW-----AKNOYAFIMRPVAVKVTSMALIAVILTSVWGATKVKDGLDITVP 706
Qy 719 RGTKEHAFSLAQRYFSLYEVALVTQGGFYAHQSQRALFDLHORFSLKAVLPPPTQAP 778
Db 707 ENTDEHEFLSRQEKYFGFYNNYVATQGNFEYPTNQKLLYEHDFVPIPIIKNDNGCLT 766
Qy 779 RTWLHYRNWLOGIQAADFQDQWASGRITRHSY-RNGSEDEGALAYKLLIQTGDAQEPDLS 837
Db 767 KFWLSLFRDWLLDLQVAFDEKVASGCTQBYWCKNASDEGLAYKLMVQTHVDNPDKS 826
Qy 838 QLTTR-KLVDREGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWHLHDKYDITGN 896
Db 827 LIATGHLVDKGLIINPKAFYNILSAMATNDALAYGASQGNLKPQQRWTHSPEDV---H 883
Qy 897 LRIPPAQLEFAQFPFLRLGLOKTDFAVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQ 956
Db 884 LEIKKSPLYITQPFYLSGLSDTXSITKLIRSVRDLCLYEAKEGPNFSPGIPFLFWEQ 943
Qy 957 YLGLRCFILLAVCILVCTFLVCAALLLNPTWAGLIVLVLMAMTVELFGIMFLGKLSA 1016
Db 944 YLYLRTSLALACALAAAFVIAVWVLLNAAVAIVTLATLVLQLLGVNALLGVKLSA 1003
Qy 1017 IPVILVASVIGVEFTVHVALGFLTTOGSNRLRAHALEHTFAPVTDGAI STLGLLML 1076
Db 1004 MEAVLLVLAIGRVHTVHLCLGFVTSIGCKRRRASLALESVAPVYVGHALAAALASML 1063
Qy 1077 AGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLSTLGPPEVIOMYKESPIILSPAP 1136
Db 1064 AASECGFVARFLRLLDIVFLGLIDGLFFPILVILGFAAEVRPI--EHPRLSTSP 1121
Qy 1137 Q-----CGGRWAGASSLPSQSFARVTTSMT 1161
Db 1122 KCSPIHPRKSSSSGGGKSSRTSKSAPRPCAPSLTIT 1160

RESULT 14

US-10-421-446-4

Sequence 4, Application US/10421446
Publication No. US20030186309A1
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
GOODRICH, LISA V
JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/421.446
FILING DATE: 22-Apr-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/724.631
FILING DATE: 28-No. US20030186309A1-2000
APPLICATION NUMBER: US/08/656.055
FILING DATE: 1996-05-31
APPLICATION NUMBER: 08/540.406
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-421-446-4

Query Match 35.6%; Score 2235; DB 14; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.5e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;

Qy 18 ARTAAPQILAGSL---KAPLWRAFYQGLLFSIGCGIQRHCGKVLFLGLAFGALALGLR 74
Db 41 AALALSELEKNEGRTSLIRAWLQEQFLILGCFLOGDAGKVLVAILVLTFCVGLK 100
Qy 75 MAIETNLEQLWVEGSRVSVQELHYTHKEKLGEAAVTSQMLIQTARQEGENILTPALGL 134
Db 101 SAQIHTRPDQLWVQEGRLAEALKYTAQALGEADSTHQLVIQAKDPDVSLHPGALLE 160
Qy 135 HLQAAALTASKVQVSLYKSGMDLNLKCYKSGVPLIEN-GMIEMWIEKLPFCVILTPDCCFW 193
Db 161 HLKVVHAARTVTHMDIENRDLDCYSPISDFEGYHHIESIDNVICAITPLDCCFW 220
Qy 194 EGAKLQGGG--AYLPQ-RPDIQNTNLDLPQLLEELG-----PFASLEGFRELLDKAQV 244
Db 221 EGSKLLGPDYPIYVPHLKHKLQWTHLNPLEVVEVKLKFQPLSTIAY---MKRAGIT 277
Qy 245 QAYVGRPCLHPDDLHCPSPAPNHHSRQAPNVAHEISGGCHGFSHKPMHWEELLGGMAR 304
Db 278 SAYMKKPCLDPTDHPCHPATAPKKSCHTIPDVAELSHGCGYFAAAAYMEWPEQLIVGGATR 337
Qy 305 DPQGLLRAELQSTFLMSPROLYEHFRGDYQTHDIGHSEQASTVLOAWORFVQLAQ 364
Db 338 NSTSALRKARLQTVVQUMGERMEYKADHYKHQIOWNEKAADVADWQKFAAEVR 397
Qy 365 EALPE--NASQOIHAFSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRW-DCAQ 420
Db 398 KITTSALRKARLQTVVQUMGERMEYKADHYKHQIOWNEKAADVADWQKFAAEVR 457
Qy 421 SOGSVGLAGVLLVALAVASGLGCLCALGITTNAAQTQVLPALGIGVDDVFLLAHAFTE 480

Db 458 SQAGVGIAGVLLSITVAAGLGCALGIPFNASSITQIVFFLAGLVQDMFLLTTHYVE 517
QY 481 ALPGTQLQRMGECLORTGTSVVLTSINNMAAFMAALVPIPALRAFSIQAAIIVGCTFV 540
Db 518 OAGDVREERTGLVKXSGSLVSLASLNCVMAFLAAALLPAPAFVFCQAALLFLNLG 577
QY 541 AVMLVFPAILSLDLRRHQRDLVLCF--SSPCSQVQIQLPQELGDGTVPGIAHLTA 598
Db 578 SILLVFPAMISLDLRRRSARADLLCLMPESP-----LPKK-----KIP----- 617
QY 599 TVQAFTHCEASSQHVVTILPPQAHVPPPSDPLGSELSPGGSTRDLGQEEETROKAA 658
Db 618 -----ERAKTRKNDKTHRIDTTRQPLDPDV-----SENVTTC 651
QY 659 KSLPCARWNLAHFARYQFAPLLIQSHAKAIVLVFGLALLGLSLYGATLVODGLALTDVVP 718
Db 652 LSVSLTKW-----AKQYAPFIMRPVAKVTSMLALIAVILTSVMGATKVKDGLDITDIP 706
QY 719 RGTHKHAFLSAQURYSLYEVALVTQGGFYAHSQRALFDLHORFSSLKAVLPPATQAP 778
Db 707 ENTDEHEFLSRQKTFGFYNNYAVTOGNFEYPTNOKLLYBYHQFVRIPNIIXNDNGGLT 766
QY 779 RTWLHYRWNLQIGQAADFQDWSAGRTTRHSY-RNGSEDCALAYKLLIOTGDAQEPDLS 837
Db 767 KFWLSLFRDWLLDLQVAFDEKVASGCITQBYWCKNASDEGILAYKLMVQIGHVDNPIKS 826
QY 838 QLTT-RKLVDREGLIPPELFYMGITVMVSSDPLGLAASQANFYPPPEWLHXYDTTGEN 896
Db 827 LITAGHLVDKDGILNPKAFYNYLSAWATNDALAYGASQGNLKPQOPQORWIHSPEDV--H 883
QY 897 LRIPPAQLEFAQFPFLRLGLOKTADEVEAIEGARAACAAGQAGVHAYPSGSPFLWEQ 956
Db 884 LEIKKSPFLYTQLPFFYLSGLSDTSIKTLIRSRVDELCLYEAKGFENFSGIPFLWEQ 943
QY 957 YLGRRCFLAVCILLVCTFLVACALLILNPNWAGLIVLVLAMMTVELFGIMGFLGKLSA 1016
Db 944 YLRTSLLLALACALAAVFIANVLLNNAWAVLVLTALATIVQLLGVNALLGVKLSA 1003
QY 1017 IPVVILVASYGIGVEFTHVALGELTTQGSRLNRAAHLEHTFAPVTDGAISTLLGLML 1076
Db 1004 MPVALLVLAIGRVHFTVHLCLGFVTSGICKRRRASLALSVLAPVVGHALAAALASML 1063
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Db 1064 AASECGFVARLEFLRLLDIVFLGLIDGLLFFPIVLISILGPAAEVRPT--EHPERLSTESP 1121
QY 1137 Q-----GGGLRWGASSLSPOSFARVTTSM 1161
Db 1122 KSPHPRKSSSSGGGDKSRTSKSAPRPCAPSLTIT 1160

RESULT 15
US-09-898-533-3
; Sequence 3, Application US/09898533
; Patent No. US20020106656A1
; GENERAL INFORMATION:
; APPLICANT: Gemmelli, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8. A GENE RELATED TO THE HEDGEHOG RECEPTOR,
; TITLE OF INVENTION: PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/898,533
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: US/09/268,140
; PRIOR FILING DATE: 2000-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1286
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-898-533-3

Query Match 31.8%; Score 1992; DB 9; Length 1286;
Best Local Similarity 37.4%; Pred. No. 8 e-155;
Matches 429; Conservative 226; Mismatches 411; Indels 80; Gaps 19;
QY 18 ARTAAPQILAGSL--KAPLWLRAYFQGLLFSIGCGIQRHCGKVLFLGLAFGALLGLR 74
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Db 94 SAQIHSKVHQLMIQEGRLAEALAYTKTIGEDESATHQLLIQTTHDPNASVHLHPQALLA 153
QY 135 HLOAALATASKVOYSLYKSKWDLNKKICYKSGVPLIEN-GMIEWIEKLFPCVILTPLDCFW 193
Db 154 HUEVLVKAIVAKVHLYDTEWGLDMCNMSTPSEFEGIIYIEQILRHILIPCSITPLDCFW 213
QY 194 EGAKLOG--GSAYLPG-RPDIOWTNLDP-----EQLLEELGPFASLEGFRELIDKAQ 242
Db 214 EGSOLLGPESAVVPIGILNORLLTTLNPASVMQYMKQKSEKISF-DFETVEQYMKRAA 272
QY 243 VGOAYVGRPCLHPDDDLHCPSPAPNHHSRQAPNVAHELSCGCHGFSHKFHWQBELILGGM 302
Db 273 IGSYMEKPCINPLNCPDTPAPNKNSTQPPDVGAILSGCYGYAAKHMHWPEELIVGGR 332
QY 303 ARDPQCELLRAEALQSTFLMSPOLYEHPRGDYQTHDICWSBEOASTVLQAWORRFVQL 362
Db 333 KNRSGHLRKAQALQSVVQMLTEKEMVDQMDNYKVHHLGWTQEKAEVLNMQNRSRE 392
QY 363 AQBALPENA---SQOIHAFSSTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRW-D 417
Db 393 VEQLLRKQSRATNYDIYVSSAALDILAKFSPSALSIVIGVAVTVLAFCTLLWRD 452
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QY 538 TFVAVMLVFPAILSLDLRRHQRDLVLCFSSPCSAQ---VTQILPQELGDGTVPGVIA 594
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QY 595 HLTAATVQAFTHCEASSQHVVTILPPQAHVPPPSDPLGSELSPGGSTRDLGQEEETRQ 654
Db 622 -----RGARHPKSCNNRVPL-----PAQNPLEQRADIPGSSHSL----- 657
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Db 658 -----ASFSLATFAFOHYTFPLMRVSVKFTVMGFLAALLISSLYASTRLQDGLII 708
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QY 775 TQAPRTWLHYRWNLQIGQAADFQDWSAGRTTRHS-YRNGSEDCALAYKLLIOTGDAQEP 833
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Qy 1071 LGLMLAGSHPDFIVRYFFAALTVTLGLLHGLVLLPVLLSIILGPPPEVIQMYKESPEI 1130
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Db 1121 ISTPSP 1126

Search completed: November 22, 2004, 08:08:02
Job time : 335 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 07:45:05 ; Search time 24 Seconds

(without alignments)
3324.190 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPRLRLPPSYTPPART.....SPATSSGNLSRRGPGATG 1203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	6272	100.0	1203	4	US-09-060-939A-2
3	6248	99.6	1203	3	US-09-207-857-2
4	6248	99.6	1203	4	US-09-309-280A-2
5	5599	89.3	1182	3	US-09-293-505-7
6	5599	89.3	1182	4	US-09-060-939A-7
7	3348	53.4	1447	2	US-08-540-406-19
8	3348	53.4	1447	3	US-08-656-055-19
9	3348	53.4	1447	3	US-08-954-668-19
10	3348	53.4	1447	3	US-09-268-140-5
11	3348	53.4	1447	4	US-08-918-658-19
12	3348	53.4	1447	4	US-09-724-631-19
13	3348	53.4	1447	4	US-08-954-701A-19
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17	3337	53.2	1434	3	US-08-954-668-10
18	3337	53.2	1434	4	US-08-918-658-10
19	3337	53.2	1434	4	US-09-724-631-10
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21	3337	53.2	1434	5	PCT-US95-13233-10
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27	2235	35.6	1311	4	US-08-918-658-4

28	2235	35.6	1311	4	US-09-724-631-4	Sequence 4, Appli
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31	1992	31.8	1286	3	US-09-268-140-3	Sequence 3, Appli
32	1961.5	31.3	1299	3	US-08-460-900C-62	Sequence 62, Appli
33	1961.5	31.3	1299	3	US-08-674-509B-48	Sequence 48, Appli
34	1961.5	31.3	1299	3	US-08-954-698-48	Sequence 48, Appli
35	1961.5	31.3	1299	4	US-09-639-695-62	Sequence 62, Appli
36	1961.5	31.3	1299	4	US-09-448-188-48	Sequence 48, Appli
37	1961.5	31.3	1299	4	US-08-954-128-48	Sequence 48, Appli
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39	1936.5	30.9	1285	2	US-08-540-406-6	Sequence 6, Appli
40	1936.5	30.9	1285	3	US-08-556-055-6	Sequence 6, Appli
41	1936.5	30.9	1285	3	US-08-954-668-6	Sequence 6, Appli
42	1936.5	30.9	1285	4	US-08-918-658-6	Sequence 6, Appli
43	1936.5	30.9	1285	4	US-09-724-631-6	Sequence 6, Appli
44	1936.5	30.9	1285	4	US-08-954-701A-6	Sequence 6, Appli
45	1936.5	30.9	1285	5	PCT-US95-13233-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-293-505-2
; Sequence 2, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-505-2

Query Match 100.0%; Score 6272; DB 3; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121	QGENILTPALGLHLQAALTAASKVQVSLYKGSWDINKTCYKSGVPLIENGMIENIEKL	180
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Db	181	FFCVILTPDLCFMEGAKQGGSAVLPGRPDIOWTNLDPELLEELGPPASLEGFRELDDK	240
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Db	301	GMARDPQGLLRARAEALQSTFLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV	360
QY	361	QLAQALPENASQOHAFFSSTLDDILHAFSEVSARVVGVLMLAYACTVMTLRWDCAQ	420

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421 SQSVGLAGVLLVALAVASGLGICALLGTTFNATTOVLPFLAIGTGVDDVFLAHAFTE 480
421 SQSVGLAGVLLVALAVASGLGICALLGTTFNATTOVLPFLAIGTGVDDVFLAHAFTE 480
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961 RRCEFLAVCILVCTFLVCALLLNPNWTAGLIVLVLAMTVELFPGIFGIKLSAIPV 1020
1021 ILVASVIGVEFTHVHAGLFTTCGSRNLRAAHLEHTFAPVTDGATSTLLGLMLAGSH 1080
1021 ILVASVIGVEFTHVHAGLFTTCGSRNLRAAHLEHTFAPVTDGATSTLLGLMLAGSH 1080
1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLSSILGPPPEVIQMYKESPEILSPAPQGG 1140
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1201 ATG 1203
1201 ATG 1203

RESULT 2

US-09-060-939A-2
; Sequence 2, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,939A
FILING DATE: 15-Apr-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1203 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-060-939A-2
Query Match 100.0%; Score 6272; DB 4; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 121 QEGENTILTEALGHLQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENTILTEALGHLQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
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Db 181 FPCVILTDCFWEGAKLQGGSAIYLPGRDPIQWNTLDPQLLEELGFPASLEGFRELDDK 240
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Db 361 QLAQALPENASQOIHAFSTTLLDDILHAFSEVSAARVVGGLMLLAYACVMTLWRWDCAQ 420
Qy 421 SQSVGLAGVLLVALAVASGLGICALLGTTFNATTOVLPFLAIGTGVDDVFLAHAFTE 480
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Qy 841 TRKLVDRGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDITTCENLRIP 900
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Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 3
US-09-207-857-2
; Sequence 2, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; FILE REFERENCE: ONV-05001
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: human
US-09-207-857-2

Query Match 99.6%; Score 6248; DB 3; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 MTRSPPLRELPPSYTPPARTAARQIILAGSLKAPLWIRAYFQGLLFSIGCGIQRHCKVLF 60
Qy 61 LGLLAFGALALGRMAIETNLBQLWVEGSRVSQELHYTKELGREAAVTSOMLIQTAR 120
Db 61 LGLLAFGALALGRMAIETNLBQLWVEGSRVSQELHYTKELGREAAVTSOMLIQTAR 120
Qy 121 QEGENILTPEALGHLQAALTASKVQVSLYKSWDLNKLICKYKSVPLIENGMIERIEKL 180
Db 121 QEGENILTPEALGHLQAALTASKVQVSLYKSWDLNKLICKYKSVPLIENGMIERIEKL 180
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Db 121 QEGENILTPEALGHLQAALTASKVQVSLYKSWDLNKLICKYKSVPLIENGMIERIEKL 180
Qy 181 FPCVILTPDLCFWEKAKLQGGSAYLPGRPDIQWNTNLDPEQLBELGPFASLEGFRELLDK 240
Db 181 FPCVILTPDLCFWEKAKLQGGSAYLPGRPDIQWNTNLDPEQLBELGPFASLEGFRELLDK 240
Qy 241 AOYGOYAVGRPCPLHPPDLHCPSPAPNHHSRQAANVAHELGGCGHSHKPMHWOEBELLG 300
Db 241 AOYGOYAVGRPCPLHPPDLHCPSPAPNHHSRQAANVAHELGGCGHSHKPMHWOEBELLG 300
Qy 301 GMARDQGEGLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEQASVLOAWORRFV 360
Db 301 GMARDQGEGLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEQASVLOAWORRFV 360
Qy 361 QLAQEAALPENASQOIHAFSSTLLDDILHAFSEVSAAARVVGYYLLMLAYACVTMLRWPCAQ 420
Db 361 QLAQEAALPENASQOIHAFSSTLLDDILHAFSEVSAAARVVGYYLLMLAYACVTMLRWPCAQ 420
Qy 421 SOGSVGLAGVLLVALAVASGLGICALLGITFNAAATTOVLPLALGIGVDDVFLAHAFTE 480
Db 421 SOGSVGLAGVLLVALAVASGLGICALLGITFNAAATTOVLPLALGIGVDDVFLAHAFTE 480
Qy 481 ALPCTPLQERMGECLQRTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
Db 481 ALPCTPLQERMGECLQRTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
Qy 541 AVMLVPPAILSLDLRRRHQORLDVLCFSSPCSAQVITQILPQELGDTVPVGHIAHTATV 600
Db 541 AVMLVPPAIFSLDLRRRHQORLDVLCFSSPCSAQVITQILPQELGDTVPVGHIAHTATV 600
Qy 601 QAFTHCEASSQHVVTILPQOAHVPPSPDPLGSELSPGSGSTRDLGQEBETKQKACKS 660
Db 601 QAFTHCEASSQHVVTILPQOAHVPPSPDPLGSELSPGSGSTRDLGQEBETKQKACKS 660
Qy 661 LPCARNLAHFAHQFAPLILQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db 661 LPCARNLAHFAHQFAPLILQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG 720
Qy 721 TKEHAFSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRSSSLKAVLPPATQAPRT 780
Db 721 TKEHAFSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRSSSLKAVLPPATQAPRT 780
Qy 781 WLHYRNWLOGIOAADFQDQWASGRITRHSYRNGSEDEGALAYKLLIQTGDAQEPDLSOLT 840
Db 781 WLHYRNWLOGIOAADFQDQWASGRITRHSYRNGSEDEGALAYKLLIQTGDAQEPDLSOLT 840
Qy 841 TRKLVDRGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDITTCENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDITTCENLRIP 900
Qy 901 PAQPLEFAQFPFLRLGLQKTADFVEAIEGARARACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
Db 901 PAQPLEFAQFPFLRLGLQKTADFVEAIEGARARACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
Qy 961 RRCFLAVCILLVCTFLVCALLLNPWTAGLIVLVLAMMTVELFGIMFGLIKLSAIPV 1020
Db 961 RRCFLAVCILLVCTFLVCALLLNPWTAGLIVLVLAMMTVELFGIMFGLIKLSAIPV 1020
Qy 1021 ILVASVIGVEFTVHVVALGFLTTQGSRLRAHAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASVIGVEFTVHVVALGFLTTQGSRLRAHAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
Qy 1081 FDFIVRYFFAALTIVLLGLLHGLVLLPVLLSILGPPPEVIQMYKSPETILSPAPQGG 1140
Db 1081 FDFIVRYFFAALTIVLLGLLHGLVLLPVLLSILGPPPEVIQMYKSPETILSPAPQGG 1140
Qy 1141 LRWGASSLPOSFARVTTSMVAIHPPPLPGAYIHPADPEPPWSPAATSSGNLSRSGPG 1200
Db 1141 LRWGASSLPOSFARVTTSMVAIHPPPLPGAYIHPADPEPPWSPAATSSGNLSRSGPG 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203
```

```
RESULT 4
US-09-909-280A-2
; Sequence 2, Application US/09909280A
; Patent No. 6605700
; GENERAL INFORMATION:
; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO. 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-280A-2

Query Match      99.6%; Score 6248; DB 4; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPILWLRAYFQGLLFSLGGCIGRHCKGVLF 60
DB      1  MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPILWLRAYFQGLLFSLGGCIGRHCKGVLF 60
QY      61  LGLAFGALALGRMAIETNLEQWVEVGSRVSOELHYTKELGEBAAVTSQMLIQATAR 120
DB      61  LGLAFGALALGRMAIETNLEQWVEVGSRVSOELHYTKELGEBAAVTSQMLIQATAR 120
QY      121  QEGENILTPALGLHQAALTASKVQVSLYKSKWDLNKKCYKSGVPLIENGMIETNLEKL 180
DB      121  QEGENILTPALGLHQAALTASKVQVSLYKSKWDLNKKCYKSGVPLIENGMIETNLEKL 180
QY      181  FPCVILTPLDCFWEGAKLQGSAYLPGRPDIQWNTLDPQLLESLGFPFASLEGFRELLDK 240
DB      181  FPCVILTPLDCFWEGAKLQGSAYLPGRPDIQWNTLDPQLLESLGFPFASLEGFRELLDK 240
QY      241  AQGVQAYVGRPCLPDHLCPGAPNHHSRQAPNVAHELGGCHGFSKFMHWQEEILLG 300
DB      241  AQGVQAYVGRPCLPDHLCPGAPNHHSRQAPNVAHELGGCHGFSKFMHWQEEILLG 300
QY      301  GMARDPOGELLRAEALQSTELLMSPROLYEHFRGDYQTHDIGNSEEOASTVLQAWQRFFV 360
DB      301  GMARDPOGELLRAEALQSTELLMSPROLYEHFRGDYQTHDIGNSEEOASTVLQAWQRFFV 360
QY      361  QLAQEALPENASQOIHAFFSTTLDLILHAFSEVSAARVWGYYLMLAYACVTMLRWDCAQ 420
DB      361  QLAQEALPENASQOIHAFFSTTLDLILHAFSEVSAARVWGYYLMLAYACVTMLRWDCAQ 420
QY      421  SQGSVGLAGVLLVALAVASGLICALLGITFNATTOVLPFLAIGIGVDVFLIAHAFTE 480
DB      421  SQGSVGLAGVLLVALAVASGLICALLGITFNATTOVLPFLAIGIGVDVFLIAHAFTE 480
QY      481  ALPGTLPQERMGECLOQTGTSVVLTSINNAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
DB      481  ALPGTLPQERMGECLOQTGTSVVLTSINNAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
QY      541  AVMLVFPAILSLDLRRHRCORLDVLCFSPSCSAQVIOIILPQELGDCGTVPVGHIAHLFATV 600
DB      541  AVMLVFPAILSLDLRRHRCORLDVLCFSPSCSAQVIOIILPQELGDCGTVPVGHIAHLFATV 600
QY      601  QAFTHCEASSQHVVTIILPQAHVLPVPSDPLGSELPFGGSTRDLQCEBETQKAAKCS 660
DB      601  QAFTHCEASSQHVVTIILPQAHVLPVPSDPLGSELPFGGSTRDLQCEBETQKAAKCS 660
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QY      661  LPCARNLHAFARYQFAPILLQSHAKAIVLVLFALLGLSLYGATLVQDGLALTDVVPRG 720
DB      661  LPCARNLHAFARYQFAPILLQSHAKAIVLVLFALLGLSLYGATLVQDGLALTDVVPRG 720
QY      721  TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
DB      721  TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRT 780
QY      781  WLHYRNWLOGIOAAFDQDQWASGRITRHSYRNSEDEGALAYKLLIQTGDAQEPLDFSQLT 840
DB      781  WLHYRNWLOGIOAAFDQDQWASGRITRHSYRNSEDEGALAYKLLIQTGDAQEPLDFSQLT 840
QY      841  TRKLVDRGLIPPELFYMGTLVWVSDPLGLAASQANFYPPPEWLHDKYDVTGGENLRIP 900
DB      841  TRKLVDRGLIPPELFYMGTLVWVSDPLGLAASQANFYPPPEWLHDKYDVTGGENLRIP 900
QY      901  PAQPLEFAQFPFLRLRGLQKTADFEVAIEGARAAACAEAGQAGVHAYTSGSPFLFWEQYLGL 960
DB      901  PAQPLEFAQFPFLRLRGLQKTADFEVAIEGARAAACAEAGQAGVHAYTSGSPFLFWEQYLGL 960
QY      961  RRCFLAVCILLVCTFLVCAILLNPNWTAGLIVLVLAMMTVELFGIMFGLIKLSAIPV 1020
DB      961  RRCFLAVCILLVCTFLVCAILLNPNWTAGLIVLVLAMMTVELFGIMFGLIKLSAIPV 1020
QY      1021  ILVASVGIGVEFVHVALGFLTTQGRNLRRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
DB      1021  ILVASVGIGVEFVHVALGFLTTQGRNLRRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
QY      1081  FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGGG 1140
DB      1081  FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGGG 1140
QY      1141  LRWGASSLSLQSPSFARVTTSMTHVHPPPLPGAVIHAPDEPPHSPANTSSGNLSSRGPG 1200
DB      1141  LRWGASSLSLQSPSFARVTTSMTHVHPPPLPGAVIHAPDEPPHSPANTSSGNLSSRGPG 1200
QY      1201  ATG 1203
DB      1201  ATG 1203

RESULT 5
US-09-293-505-7
; Sequence 7, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ. ID NO. 7
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-293-505-7

Query Match      89.3%; Score 5599; DB 3; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

QY      1  MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPILWLRAYFQGLLFSLGGCIGRHCKGVLF 60
DB      1  MVRPLSLGELPPSYTPPARTAAPQILAGSLKAPILWLRAYFQGLLFSLGGCIGRHCKGVLF 60
QY      61  LGLAFGALALGRMAIETNLEQWVEVGSRVSOELHYTKELGEBAAVTSQMLIQATAR 120
DB      61  LGLAFGALALGRMAIETNLEQWVEVGSRVSOELHYTKELGEBAAVTSQMLIQATAR 120
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121 QEGENILTPALGLHLQAALTASKVQSVLYGKSWDLNKKIYKSGVPLIENGMIEMIEKL 180
121 QEGENVLTPEALDLHLQAALTASKVQSVLYGKSWDLNKKIYKSGVPLIENGMIEMIEKL 180
181 FPCVILTPDLCFWEKAGLQGSAYLPGRDPIQWNTLDPQLLEELGPFASLEGFRELDDK 240
181 FPCVILTPDLCFWEKAGLQGSAYLPGRDPIQWNTLDPQLLEELGPFASLEGFRELDDK 240
241 AOVGOAYVGRPCPLHPDDLCPAPNHHRSQAPNVAHELSGGCHGFSHKFMHQBELLG 300
241 AOVGOAYVGRPCPLDPDPCHCPAPNHHRSQAPNVAHELSGGCHGFSHKFMHQBELLG 300
301 GMARDPQGLLRALAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLAQWRRFV 360
301 GTARDLQGLLRALAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLAQWRRFV 360
361 QLAQEALPENASQOIHAFFSTTLLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
361 QLAQEALPANASQOIHAFFSTTLLDDILHAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420
421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATTOVLFPFALGIGVDDVFLAHAFTE 480
421 SQGAVGLAGVLLVALAVASGLGICALLGITFNAAATTOVLFPFALGIGVDDVFLAHAFTE 480
481 ALPGTLPQERMGCLOKRTGTSVLTSTINNAAFIAMAALVPIPALRAFSLOAAIVVGCTFV 540
481 APDPTLPERMGCLOKRTGTSVLTSTINNAAFIAMAALVPIPALRAFSLOAAIVVGCTFV 540
541 AVMLVFPAILSLDRRHRQRDLVLCFSSPCSAQVITQILPQBLGDCGTVPGIAHLTATV 600
541 AVMLVFPAILSLDRRHRQRDLVLCFSSPCSAQVITQILPQBLGDCGTVPGIAHLTATV 600
601 QAFTHCEASQHVVTLLPQAHVLPVPPDPLGSELSPGSTRDLQGBEETKQKAACKS 660
601 QAFTHCEASQHVVTLLPQAHVLPVPPDPLGSELSPGSTRDLQGBEETKQKAACKS 660
661 LPCARWLHAFARYQAPILLOSHAKAIVLVLPFALLGLSLYCATLVQDGLATDVVPRG 720
661 LLCAHWTLHAFARYQAPILLOSHAKAIVLVLPFALLGLSLYCATLVQDGLATDVVPRG 720
721 TKEHAFSLAQLRYESLYEVALVTQGGFDYAHSQALFDLHQRFSLSKAVLPPPPATQAPT 780
721 TKEHAFSLAQLRYESLYEVALVTQGGFDYAHSQALFDLHQRFSLSKAVLPPPPATQAPT 780
781 WLHYRNWLGIOQAADFQDOWASGRITRHSYRNGSEGCALAYKLLIQTGDAQEPDLSOLT 840
781 WLHYRNSWLGIOQAADFQDOWASGRITRHSYRNGSEGCALAYKLLIQTGDAQEPDLSOLT 840
841 TRKLVDREGLIPPELFWGLTVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
841 TRKLVDREGLIPPELFWGLTVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
901 PAQPLEFAQFPFLRLGLOKTDVFEALLEGARAAACAEAGQAGVHAYFSGSPFLFWEQYGL 960
901 PAQPLEFAQFPFLRLGLOKTDVFEALLEGARAAACAEAGQAGVHAYFSGSPFLFWEQYGL 960
961 RRCFLAVACILLVCTFLVCAILLNFWTAGLIVLVLAMTVELFGIMFLGIKLSAIPVV 1020
961 RRCFLAVACILLVCTFLVCAILLNFWTAGLIVLVLAMTVELFGIMFLGIKLSAIPVV 1020
1021 ILVASVIGVEFTVHVALFLLTQGSNLRRAHALEHTFAPVTDGALSTLLGLMLAGSH 1080
1021 ILVASVIGVEFTVHVALFLLTQGSNLRRAHALEHTFAPVTDGALSTLLGLMLAGSH 1080
1081 FDPVIRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPELSPAPQGGG 1140
1081 FDPVIRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPELSPAPQGGG 1140
1141 LRWGASSLUPQSFARVTTMTVAIHPPPLPGAYIHPADPEP 1181
1141 LRWDRPPTLPQSFARVTTMTVAIHPPPLPGAYIHPADPEP 1181

RESULT 6

US-09-060-939A-7
; Sequence 7, Application US/09060939A
; Patent No. 670938
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Minipac (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-060-939A-7

Query Match 89.3%; Score 5599; DB 4; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

QY 1 MTRSPLERLPSPYTPPARTAPOIILAGSLKAPLWLRAYFOGLLSLGGIQRHCGKVLFP 60
Db 1 MVRPLSLGELPPSYTPPARSSAPHILLAGSLQAPLWLRAYFOGLLSLGGIQRHCGKVLFP 60
QY 61 LGLLAFGALALGLRMAIETNLEQLWVEVGSRSVQELHYTKELGEEAAVTSQMLIQTAH 120
Db 61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRSVQELHYTKELGEEAAVTSQMLIQTAH 120
QY 121 QEGENILTPALGLHLQAALTASKVQSVLYGKSWDLNKKIYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENVLTPEALDLHLQAALTASKVQSVLYGKSWDLNKKIYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDLCFWEKAGLQGSAYLPGRDPIQWNTLDPQLLEELGPFASLEGFRELDDK 240
Db 181 FPCVILTPDLCFWEKAGLQGSAYLPGRDPIQWNTLDPQLLEELGPFASLEGFRELDDK 240
QY 241 AOVGOAYVGRPCPLHPDDLCPAPNHHRSQAPNVAHELSGGCHGFSHKFMHQBELLG 300
Db 241 AOVGOAYVGRPCPLDPDPCHCPAPNHHRSQAPNVAHELSGGCHGFSHKFMHQBELLG 300
QY 301 GMARDPQGLLRALAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLAQWRRFV 360
Db 301 GTARDLQGLLRALAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLAQWRRFV 360
QY 361 QLAQEALPENASQOIHAFFSTTLLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
Db 361 QLAQEALPANASQOIHAFFSTTLLDDILHAFSEVSTTRVVGGYLLMLAYACVTMLRWDCAQ 420
QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATTOVLFPFALGIGVDDVFLAHAFTE 480
Db 421 SQGAVGLAGVLLVALAVASGLGICALLGITFNAAATTOVLFPFALGIGVDDVFLAHAFTE 480

QY 481 ALPGTLPORMGECLOQTCTSVLTSINMAAFIPALRAFSLOAAIVVGCTFV 540
Db 481 APDPTLPERMGCRLSTGTSVLTSSNNVMAAFIPALRAFSLOAAIVVGCTFV 540
QY 541 AVMLVPAIISLDLRRHRCORLDVLCFSSPCSAQVITQILPQELGDCGTPVGVIAHTATV 600
Db 541 AVMLVPAIISLDLRRHRCORLDVLCFSSPCSAQVITQILPQELGDCGTPVGVIAHTATV 600
QY 601 QATHCASSQHVVTILPPOAHIVPPSDPLGSELPSPGGSTRDLGQEBETKQKAACKS 660
Db 601 QATHCASSQHVVTILPPOAHIVPPSDPLGSELPSPGGSTRDLGQEBETKQKAACKS 660
QY 661 LPCARNLAFHAFYQAPLILQSHAKAIVLFGALLGLSLYCATIVODGLATDVVPRG 720
Db 661 LLAHWTLAFHAFYQAPLILQSHAKAIVLFGALLGLSLYCATIVODGLATDVVPRG 720
QY 721 TKEHAFSLAQRYFSLSYEVALVTQGGPDYAHSQRALFDLHQRFFSSLKAVLPPPATQAPRT 780
Db 721 TKEHAFSLAQRYFSLSYEVALVTQGGPDYAHSQRALFDLHQRFFSSLKAVLPPPATQAPRT 780
QY 781 WLHYRNWLOGIOAAFDQDQWASGRITHSYRNGSEDCALAYKLLIQGDAQEPIDFSQLT 840
Db 781 WLHYRNWLOGIOAAFDQDQWASGRITHSYRNGSEDCALAYKLLIQGDAQEPIDFSQLT 840
QY 841 TRKLVDREGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDREGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY 901 PAOPLEPAQFPFLRLGLQKTADEVEALEGARAACAEAGAGVHAYPSGSPFLFWEQYLG 960
Db 901 PAOPLEPAQFPFLRLGLQKTADEVEALEGARAACAEAGAGVHAYPSGSPFLFWEQYLG 960
QY 961 RRCPELLAVCTILVLCALLLNPNWTAGLIVLVLAMTVELFGIMFGIKLSAIPV 1020
Db 961 RRCPELLAVCTILVLCALLLNPNWTAGLIVLVLAMTVELFGIMFGIKLSAIPV 1020
QY 1021 ILVASIGVGEFTVHVALGTLTQGSNLRANAALHTFAPVTDGALSTLGLMLAGSH 1080
Db 1021 ILVASIGVGEFTVHVALGTLTQGSNLRANAALHTFAPVTDGALSTLGLMLAGSH 1080
QY 1081 FDFIVRYFAALVTLLGLLHGLVLLPVLISILGPPPEVIQMYKESFETILSPAPQGG 1140
Db 1081 FDFIVRYFAALVTLLGLLHGLVLLPVLISILGPPPEVIQMYKESFETILSPAPQGG 1140
QY 1141 LRWASSLPSQFARVTTMTVAIHPPPLPGAVIHPADPEP 1181
Db 1141 LRWASSLPSQFARVTTMTVAIHPPPLPGAVIHPADPEP 1181

RESULT 7

US-08-540-406-19
; Sequence 19, Application US/08540406
; Patent No. 5837538
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-540-406-19

Query Match 53.4%; Score 3348; DB 2; Length 1447;

Best Local Similarity 49.9%; Pred. No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFLSLGCGIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAFALQISKGKATGRKAPLWLRKAFQRLFLKLCYIQKNGKELVVGLLIFGA 111
QY 69 LAIGLRLMAIETWELQWVGVSRVQELHYTTEKLGEEAAYTSQMLIQARQENILT 128
Db 112 FAYGLKAANLETVVEELWVGVRVSRVRELNYTRQKIGEEAMPNQLMIQTPKEEGANVLT 171
QY 129 PEALGHLOALATASKVQVSLYCKSDLNKICVKSGVPLEENGMIMWIKLPCPVLTLP 188
Db 172 TEALLQHLDSALQASRVHVYNNRQWKLHLCKYKSGELITETGYNOQIIBYLPCLITP 231
QY 189 LDCFWEGAKLQGGSAYLPGRPDIQWNLDPQLLEELGPF-ASDEGFRELLDKAQVQAY 247
Db 232 LDCFWEGAKLQSGTAVILGKPLRWTFDFLEELKKNYQVDSWEEMLNKAEVGHY 291
QY 248 VGRPCLHPDDLHPPGAPNHSRQANVAHELGGCHGSHKFMHWQEEILLGGMARDPQ 307
Db 292 MDRPCLNPADPCPATPNKNTKPLDMALVNLGGCHGLSRKRMHWQEEILLGVTENST 351
QY 308 GELLRAEALQSTELLMSPROLYEHFRG-DYCTHDIGWSEBQASTVLQAWORRFVQLAQEA 366
Db 352 GKLVSAHALQTMFLMTPKQMYEHFKGYEVSH-INWEDKAAALEAWORTYVEVYHQS 410
QY 367 LPENASQQIHAFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQSQSVG 426
Db 411 VAQNSTQKVLSTFTTTLLDILKSFSDSVIRVASGYLLMLAYACLIMLRWDCSKSQAVG 470
QY 427 LAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLAHAFTEALPG-- 484
Db 471 LAGVLLVALSVAAGLGLCSLIGISFNAAATQVLPFLALGIGVDDVFLAHAFSETQNK 530
QY 485 TPLQERMGECLQRTGTSVLTSSNNMAAFIPALRAFSLOAAIVVGCTFVAVML 544
Db 531 IPEDRTGECCKRTGASVALTSNVTAFPMALIFIPALRAFSLOAAIVVFNFAVLL 590
QY 545 VFPAILSLDLRRRRHRCORLDVLCFSSPCSAQVITQILPQELGDCGTPVGVIAHTATV 595
Db 591 IFFAILSMIDLYRREDRLDIFCCFTSPCVSRVQVPEQAYTDTHTNTRYSPPPYSSHSF 650
QY 596 -----LATVQAFTHCEASSQHVVTILPPOAHIVPPP-----SDPLGSELPSPGGSTRD 644
Db 651 AHETQITMQSTVQLRTEYDPTHTVYTTABPREISVQPVVTQDLSLSCQSPSTSTRD 710
QY 645 LLGQEBETROKAAACKSLPCARNLAFHAFYQAPLILQSHAKAIVLFGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPPTCKWTLSFAEKYHAFPLKPKAKVVVIFLGLLGVSLYGT 768
QY 705 TLVQDGLALTVDVVRGTKEHAFSLAQRYFSLSYEVALVTQGGPDYAHSQRALFDLHQRFFSS 764

Db 769 TVRDLGLDLDIVPRETREVDFIAAQKFYFYNMVIYVTKA-DYENIQHLLYDLHRSFS 827
QY 765 SLKAVLPPTAQAPRTWLYHYNWLMGIIQAADFQDWASGRITRHSYRNGSEDEGALAYKLL 824
Db 828 NVKYVMLEENKQPKMWLHYFRDMLQGLQDAPDSWETKIMPNYKNGSDGGLAYKLL 887
QY 825 IOTGDAQEPLDPSOLTRKLVOREGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPE 884
Db 888 VQTGSRDKPIDISQLTKQLRVDAGDGIINPSAFIYLTAWVNSDPVAYAAQANIRPHRE 947
QY 885 WLHDKYDTTGE-NLRIPPAQLEFAQFPFLRLGLQKTADFEVAIEGARAACARAGQGVH 943
Db 948 WYHDKADYMPETELRIPAAEPIEYAFYFYLNGLRUTSDFEVAIEKVRTICSNYTSLGLS 1007
QY 944 AYPGSGFFLFWEOYLGLRCLLAVCILVCTPLVLCALLLNLPWTAGLIVLVLMVTVEL 1003
Db 1008 SYNGYFFLFWEOYLGLRCLLAVCILVCTPLVLCALLLNLPWTAGLIVLVLMVTVEL 1067
QY 1004 FGIMGFLGKLSAIPVILVASVIGVETVHVVALGFLTTGSRNLRAAHLEHTEAPVT 1063
Db 1068 FGMGGLGKLSAIPVILVASVIGVETVHVVALGFLTTGSRNLRAAHLEHTEAPVT 1127
QY 1064 DGAISTLLGLMLAGSHFDFIVRYFFAALTLLGLLHGLVLLPVLLSLTGPPPEVI-- 1121
Db 1128 DGAISTLLGLMLAGSHFDFIVRYFFAALTLLGLLHGLVLLPVLLSLTGPPPEVI-- 1187
QY 1122 QMYKSGPE-----ILSP-----APQG 1139
Db 1188 NGLNRLPTSPPEPPSVRFAMPFGHSGSDSSSEYSSQTTVSGLSBELRHYEAQGA 1247
QY 1140 G-----LRWG-----ASSLSQSFAR 1155
Db 1308 REGMLPPLVPRDFAFEISTEGHSGSNRARMGPRGARSHNPNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAVIHP 1176
Db 1368 ITVTASASVTVAHPPVPGGRNP 1393
RESULT 8
US-08-656-055-19
; Sequence 19, Application US/08656055
; Patent No. 6027882
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,055
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/540,406
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-055-19
Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
QY 12 PSYTPPARTAAPOILAGSL---KAPLWIRAYFQGLIFSLGCGIQRHCGKVLFLGLILAFGA 68
Db 53 PSYC-DAAPALEQISKGATGRKAPLWIRAKFQRLFKLGCYIQKNCGRFLVVGLLIFGA 111
QY 69 LALGLRMALITETNLEQLWVEGSRVSOELHYTKKELGEEAAVTSOMLIOTARQEGENILT 128
Db 112 FAVGLKAANLETNVELWVEGSRVRELYNTRQKIGEEAMFPQMIQTPKEEGANVLT 171
QY 129 PEALGHLQAALTASKVQVSLYKGSMDLNKICYKSGVPLIENGMIEMIEKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHVYMYNRQMKLEHLCYKSGELITETGYMQIIEYLPCLIIIP 231
QY 189 LDCFWEKAKLGGSAVLPGRPIQWNTLNDEQLLELPGF-ASLEFRELLDKAQVQAY 247
Db 232 LDCFWEKAKLGGSAVLPGRPIQWNTLNDEQLLELPGF-ASLEFRELLDKAQVQAY 291
QY 248 VGRPLHPDDLHCPPSPNHHRSRQAPNAHLSGGCHGFSGKFMHWOELLICGMARDPQ 307
Db 292 MORPCLNPAADPCPATAPNKNSTKPLDMALVINGCHGLSRKYMHWQELIIVGTVKNST 351
QY 308 GELLRAELAQSTFLMSRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRFRVQLAQBA 366
Db 352 GKLVSAHALQTMFQMLTPKQMYEHPKGYEVSH-INWNEKAAAILLEAQRTYVEVHQS 410
QY 367 LPENASQIHTAFSSTLDDILHAFSEVSAARVVGVLMLAYACVATMLRWDCAQSGSVG 426
Db 411 VAQNSTQKVLSPFTTTTLLDDILKSPSDSVIRVASGVLLMAYACVATMLRWDCAQSGSVG 470
QY 427 LAGVLLAVASGLGLCALIGITENAAATTVLPALGIGVDDVFLLAHAFTEALPG-- 484
Db 471 LAGVLLAVASGLGLCALIGITENAAATTVLPALGIGVDDVFLLAHAFTEALPG-- 530
QY 485 TPLQERMGECLQRTGTSVVLTISINNAAFILMAALVPIPALRAFSLQAAIVGCTFVAVML 544
Db 531 IPPEDRTGECLKRTGASVALTSISNVTAFMAALIPIPALRAFSLQAAIVVFNFAVLL 590
QY 545 VFPAILSLDLRRHCOBLDVLCCFSPSCSAQVILQBELD-----GTVPVGAH-- 595
Db 591 IFFAILSLMDLYRRDRRLDIFCCFTSPCVSVIQVEPQAYTDTHTNTRYSPPPYSSHSF 650
QY 596 -----LTATVQAFTHCEASSQHVVTILPPOAHVLPPP-----SDPLGSELSPGGSTRD 644
Db 651 AHETQITMSTVQLRTEYDPHTHYTTAEPSKSEISVQVTVTQDTLSCQSPSTSTRD 710
QY 645 LLGQEEETRQKAAKSLPCARWNLAHFARYQFAPLLQLSHAKAIVLVFLGALLGLSLYGA 704
Db 711 LLSQSFDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVWVIFLGLLGVSLYGT 768
QY 705 TLVQDGLALTVDVPRGTKEHAFLSAQLRYFSYIEVALVTQGGFDVAHSORALFDLHQRFS 764
Db 769 TRVRDGLDLDIVPRETREVDFIAAQKFYFYNMVIYVTKA-DYENIQHLLYDLHRSFS 827
QY 765 SLKAVLPPTAQAPRTWLYHYNWLMGIIQAADFQDWASGRITRHSYRNGSEDEGALAYKLL 824

Db 828 NVKYMVLEENKQLPKWMLHYFRDWMLOGLQDAFSDWETKIMPNYKNGSDDGVLAYKLL 887
 QY 825 IQTGDAQEPLDFSLTRTKLVDRGLPPELFYMGTLVWVSSDPLGLAAQANFYPPPE 884
 Db 888 VQIGSRDKPIDISQTKQRLVDADGIINPSAFIYLTAWVSNDDPVAARQANIRHRPE 947
 QY 885 WLHDKYDTTGE-NLRIPPAQPLEFAQPPFFLLRGLQKTADFEVATEGARAACAAGQAGVH 943
 Db 948 WVKDKADYMPETRLRIPAAEPVIAQPPFYNGLRDTSDFEALKEKVTICSNYTSGLS 1007
 QY 944 AYSGSPFLFWQVGLRURFLAVCLLVCTFLVLCALLINPWTAGLIVLVAMMTVEL 1003
 Db 1008 SYNGYPLFWQVGLRURFLAVCLLVCTFLVLCALLINPWTAGLIVLVAMMTVEL 1067
 QY 1004 FGMWFGIGIKLSAIPVIVLASVIGVGFVTHVALGFLTTQGSNLRRAAHLEHTFAPVT 1063
 Db 1068 FGMWFGIGIKLSAIPVIVLASVIGVGFVTHVALGFLTTQGSNLRRAAHLEHTFAPVT 1127
 QY 1064 DGAISTLLGLLAGSHFDIVRYFFAALTTLTLGLLHGLVLLPVLLSILGPPPEVI-- 1121
 Db 1128 DGAISTLLGLLAGSHFDIVRYFFAALTTLTLGLLHGLVLLPVLLSILGPPPEVI-- 1187
 QY 1122 ----QMYKESPE-----ILSP-----APQGG 1139
 Db 1188 NGLNRLFTPSPEPPPSVVRPAMPFGHTHSGSDSDSEYSSQTTVSGLSEELRHVEAQA 1247
 QY 1140 G-----LRWG-----ASSLIPQSFA 1155
 Db 1248 GGAHQVIVTEATNPVFAHSTVHPESRHHPNPROOPHLDSGLPPGQGGQRRDPP 1307
 QY 1141 -----LRWG-----ASSLIPQSFA 1155
 Db 1308 REGMLPPLXPRRDAFEISTEGHSGPSNRARWGRGRARSHNPRNPASTAMGSSVPGVCQP 1367
 QY 1156 VTT-----SMTVAIHPPPLDGAIVHP 1176
 Db 1368 ITTWTASATVAVHPPVPGGRNP 1393

RESULT 9

US-08-954-668-19
 ; Sequence 19, Application US/08954668
 ; Patent No. 6172200
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V
 ; APPLICANT: JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley, Hoag & Eliot
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII(text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/954,668
 ; FILING DATE: 20-Oct-1997
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36709
 ; REFERENCE/DOCKET NUMBER: SUV-003.06
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1447 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-954-668-19
 Query Match 53.4%; Score 3348; DB 3; Length 1447;
 Best local similarity 49.9%; Pred. No. 1.7e-314;
 Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
 QY 12 PSYTPARTAAPQILAGSL---KAPLWLRAYFOGLLFSLCGCIQRHCGKVLFLGLLAFGA 68
 Db 53 PSYC-DAAPALEQISGKATGRKAPLWLRKAFORLLFKLCYIQKNGCKFLVGLLIFGA 111
 QY 69 LALGLRWAIETNLELWVEVGRVSRVSOELHYTKKIEGEEAAYTSQMLIQTARQEGENILT 128
 Db 112 FAVGLKAANLETNVEELWVEVGRVSRVRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLT 171
 QY 129 PEALGLHLQAALTASKVQVSLYKSWDLNKKICYKSGVPLIENGMIEMWIEKLPFCVILTP 188
 Db 172 TEALLOHLSALQASRVHVYMYNRQMKLEHLCKYSGELITETGYMDQIIEYLPCLLIITP 231
 QY 189 LDCFWEGAKLQGSAYLPGRPDIQWNTNLDPEOLLEELGPF-ASLEGPRELIDRAQVGOAY 247
 Db 232 LDCFWEGAKLQGSAYLPGRPDIQWNTNLDPEOLLEELGPF-ASLEGPRELIDRAQVGOAY 291
 QY 248 VGRPCLHPDDLHCPSPAPNHHSRQAPNVAHELGGCHGFSHKPMHMQEELLGLGMARDPQ 307
 Db 292 MDRPCLNPADPCPATAPNKNSTKPLDMALVINGCHGLSRKYMHHMQEELLIGTVKNST 351
 QY 308 GELLRAEALQSTFLIMSPQLYEHPRG-DYQTHDIGWSEQASTVLAQWRPVQLAQEA 366
 Db 352 GKLVSAHALQTMFQMLTPKQMYEHFGYEVSH-INWNEDKAAAILAEWQRTVEVHVQS 410
 QY 367 LPENASQQLHAFSSTTDDILHAFSEVSAARVGVGYLLMLAYACTVLMRWDCAQSGSVG 426
 Db 411 VAQNSTQKVLSTFTTILDDILKSFSDSVIRVASGYLLMLAYACLTLRWDCSKSQAVG 470
 QY 427 LAGVLLVALAVASGLGCLCALLGTFNAATQVLPFLALGIGVDVDFLLAHAFTEALPG-- 484
 Db 471 LAGVLLVALSVAAGLGLSLGIFSNAATQVLPFLALGIGVDVDFLLAHAFSETQNK 530
 QY 485 TPLQERMGELQRTGTSVLTISINNAEFLMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
 Db 531 IPFEDTGECLKRTGASVALTISINVTAFPMALIPALRAFSLQAAIVVGCTFVAVML 590
 QY 545 VFPAILSLDLRRRRCORLVLCCFSPCSAQVQIILPOELGD-----GTVPVGIAT-- 595
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 QY 596 -----LTATVQAFTHCEASSQHVVTILPPQAHVPPP-----SDPLGSELSPGSGSTRD 644
 Db 651 AHETQITMQSTVQLRTEYDPHTHYVYTTAEPRSEISVQPVVTQDTLSQCSPESTSTRD 710
 QY 645 LLGOEEETQKAAKSLPCARWNLAFARYQAPLLOSHAKAIVLVLCALLGLSLYGA 704
 Db 711 LLSQFSDS--SLHCLPEPCTKMTLSSFAEKHYAPFLKPKAKVVFVIFLGLLGLVSLYGT 768
 QY 705 TLVQDGLALTVDVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYAHORALFDLHORFS 764
 Db 769 TRVRDGLDLTDIVPRETREVDFIAQOFKYFSFNWYIVTQKA-DYFNIQHLLYDLHRSTS 827
 QY 765 SLKAVLPPPATQAPRTWLHYRNWLOGIQAAFDQDQWASGRITRHSYRNGESEDGALAYKLL 824
 Db 828 NVKYMVLEENKQLPKWMLHYFRDWMLOGLQDAFSDWETKIMPNYKNGSDDGVLAYKLL 887
 QY 825 IQTGDAQEPLDFSLTRTKLVDRGLPPELFYMGTLVWVSSDPLGLAAQANFYPPPE 884
 Db 888 VQIGSRDKPIDISQTKQRLVDADGIINPSAFIYLTAWVSNDDPVAARQANIRHRPE 947
 QY 885 WLHDKYDTTGE-NLRIPPAQPLEFAQPPFFLLRGLQKTADFEVATEGARAACAAGQAGVH 943

Db 948 WVDKADYMPETRLRIPAEPIEYAOFPFVINGLROTDSEVEAIEKVRTICSNYTSLS 1007
QY 944 AYPGSPFLFMEQYGLRRCFLAVALCILLVCTELVCALLLNPNWTAAGLIVLVLAMTVEL 1003
Db 1008 SYNGYPFLFMEQYIGLRHLLLFISVWLACTELVCAVFLNPNWTAAGIIVMVLAMTVEL 1067
QY 1004 FGTMGFLGIKLSAIPVILVASVIGVEFVHVHVALGFLITQGSNLRAAHALHETAPVT 1063
Db 1068 FGMGLIGIKLSAVPVILVASVIGVEFVHVHVALGFLITQGSNLRRAVLALEHMFAPVL 1127
QY 1064 DGAISTLLGLLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLLSLILGPPPEVI-- 1121
Db 1128 DGAISTLLGLVLMAGSEDFIVRYFFAVLAILIILGVINGLVLPLVLLSFFGYPPEVSPA 1187
QY 1122 ----QMYKSPE-----ILSP-----APQGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRFAMPFGHGTSGSDSEYSSQTTVSGLSEELRHYEAQOGA 1247
QY 1140 G-----LRWG----- 1140
Db 1248 GGAHQVIVEATENPVFAHSTVVHPSRHHPPSNRQPHLDGSLPPGSGQQRDRPP 1307
QY 1141 ----- 1141
Db 1308 REGIWPPLYRPRDAFEISTEGHSGPSNRARWGPARGARSHNPRNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITTWTASAVTVAVHPPVPVPGGRNP 1393
RESULT 10
US-09-268-140-5
; Sequence 5, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-268-140-5
Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
QY 12 PSYTPPARTAAPQILAGSL---KAPLWRAIFYGQLLFSLGCIGIQRHCGKVLFTGLLAFGA 68
Db 53 PSYC-DAAPALEQISKGATGRKAPLWRAKFORLLFKLCYIQKNCCKFLVVGLLIFGA 111
QY 69 LAIGLRMAIETNLEQLWVEGSRVSOELHYTKELGSEAAVTSOMLIQTARQEGENILT 128
Db 112 FAVGLKAANLETVNEELWVGVRVSRVRELNYTRQKIGEEAMFNPQMIQTPEGANVLT 171
QY 129 PEALGLHQAALTASKVOVSLYKGSWDLNKKIKYSGVPLIENGMIEMIEKLPCCVILTP 188
Db 172 TEALLQHLDSALQASRVHVYVYRWQKLEHLCYKSGELITETGVMQIIEYLPCLILTP 231
QY 189 LDCFWEGAKLQGSAYLPGRPDIQWNTLDPQLLELGPFF-ASLEGPRELLDKAQVQAY 247
Db 232 LDCFWEGAKLQSGTAYLLGKPLLRWTNFDPLFLEELKKNYQVDSWEEMLNKAEVGHY 291

QY 248 VGRPCPLHDDLHCPSPAPNHSRQAPNVAHELSCGCHGFESHKEFMHWOELLILGGMARDPQ 307
Db 292 MORPCNLPADPDPCATAPNKNSTKPLDMLVNLGGCHGSRKYMHWOELLIVGGTVKNST 351
QY 308 GELLRAEALQSTPFLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWORRERVLQAE 366
Db 352 GKLVSAHALQTMFQMLTPKQMYEHFKGYEVSH-INWNEDKAAALAEAMQRTVEVHQS 410
QY 367 LPENASQIHAHSSSTLDDILHAFSEVSAARVVGGLMLLAYACVYMLRWDCAQSGSVG 426
Db 411 VAQNSTQKVLSTFTTTTDDILKSFSDSVIRVASGYLLMLLAYACLTMLRWDCKSGQAGV 470
QY 427 LAGVLVALAVASGLGICALLGITENAAATOVLPALGIGVDDVFLAHAFETALPG-- 484
Db 471 LAGVLVALAVASAGLGLSISFNAAATQVLPALGVDDVFLAHAFSETGONKR 530
QY 485 TPLQERMGELQRTGTSTSVVLTISNNMAAFMLAALVPIPALRAFSLQAAIIVGCTFVAVML 544
Db 531 IPEEDRTGELKRTGASVALTSISNVTAFMAALIPALRAFSLQAAVAVVVFANVLL 590
QY 545 VFPAILSLDLRRHRCORLQVLCCFSPCSAQVLIQILPOELGD-----GTVPVGAH-- 595
Db 591 IFFAILSLMDLYRREDRLDIFCFTSPCVSRVQVPEQAYTDTHTDNTRYSPPPYSHSF 650
QY 596 -----LTATVQAFTHCEASSQHVVTILPPQAHVPPP-----SDPLGSELFPSSGSTRD 644
Db 651 AHETQITMSTVQLRTYDHPHTHYTTAPRSEISVQPVTVTQDTLSCOSPESTSTRD 710
QY 645 LLGQEBETRQKAAKSLPCARMNLAHFARYQFAPLLIQSHAKAIVLFLGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPEPCTKWLTLSSFAEKHYAPFLKPKAKVVVFLFLGLLGVSLYGT 768
QY 705 TLVQDGLALTVDVPRGTKEHAFLSAOLRYFSLYEVALVTQGGEDYAHSGRALLFDLHQRF 764
Db 769 TRVRDGLDLTDIVPRETREYDFIAQKFYSFYNMIVTQKA-DYPNIQHLLYDLHRSFS 827
QY 765 SLKAVLPPATQAPRTWLHYRNWLOGIOAAFDQDNASGRI TRHSYRNSEDCALAYKLL 824
Db 828 NVKYVWLEENKQLPKRWLHYFRDMLQGLQDAFDSMETGKIMPNYKNGSDGGLAYKLL 887
QY 825 IQGTDAQEPLDFSQLTRKLVDRREGIIPPELFYMLGTVMVSSDPLGLAASQANFYPPPE 884
Db 888 VQTGRDQKPIDISQTLKQRLVDADGIINPSAFIYLTAWVNDPVAVASQANIRHPPE 947
QY 885 WHDKYDVTGR-NLRIPPAQPLEPFAOPFLLRGLQKTADVEAIEGARAACAAGQAGVH 943
Db 948 WHDKADYMPETRLRIPAEPIEYAOFPFVINGLROTDSEVEAIEKVRTICSNYTSLS 1007
QY 944 AYPGSPFLFMEQYGLRRCFLAVALCILLVCTELVCALLLNPNWTAAGLIVLVLAMTVEL 1003
Db 1008 SYNGYPFLFMEQYIGLRHLLLFISVWLACTELVCAVFLNPNWTAAGIIVMVLAMTVEL 1067
QY 1004 FGTMGFLGIKLSAIPVILVASVIGVEFVHVHVALGFLITQGSNLRRAVLALEHETAPVT 1063
Db 1068 FGMGLIGIKLSAVPVILVASVIGVEFVHVHVALGFLITQGSNLRRAVLALEHMFAPVL 1127
QY 1064 DGAISTLLGLLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLLSLILGPPPEVI-- 1121
Db 1128 DGAISTLLGLVLMAGSEDFIVRYFFAVLAILIILGVINGLVLPLVLLSFFGYPPEVSPA 1187
QY 1122 ----QMYKSPE-----ILSP-----APQGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRFAMPFGHGTSGSDSEYSSQTTVSGLSEELRHYEAQOGA 1247
QY 1140 G-----LRWG----- 1140
Db 1248 GGAHQVIVEATENPVFAHSTVVHPSRHHPPSNRQPHLDGSLPPGSGQQRDRPP 1307
QY 1141 ----- 1141
Db 1308 REGIWPPLYRPRDAFEISTEGHSGPSNRARWGPARGARSHNPRNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176

Db 1368 ITTVTASASVTVAHPHPPVPGGRNP 1393

RESULT 12

US-09-724-631-19

; Sequence 19, Application US/09724631

; Patent No. 6551782

; GENERAL INFORMATION:

; APPLICANT: SCOTT, MATHEW P

; GOODRICH, LISA V

; JOHNSON, RONALD L

; TITLE OF INVENTION: Patched Genes and their Use

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: US

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/724,631

; FILING DATE: 28-No. 6551782-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/656,055

; FILING DATE: 1996-05-31

; APPLICATION NUMBER: 08/540,406

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertram I

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: a60190-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1447 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-724-631-19

Query Match 53.4%; Score 3348; DB 4; Length 1447;

Best Local Similarity 49.9%; Pred. No. 1.7e-314;

Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPARTAPQILAGSL---KAPLWIRAYFQGLFLFSLGCGIQPHCGKVLFLGLLAFGA 68

Db 53 PSYC-DAAFALBQISGKATGRKAPLWIRAKFQRLFLKGCYIQKNCCKFLWGLLIFGA 111

QY 69 LALGLRMAITETNLEQLWVEGSRVSOBLHYTKELGEEAAVTSQMLIQATAROGENILT 128

Db 112 FAVGLKAANLTVNEELWVEGSRVSELNVTROKIGEEAMFNQMLWQIPKPEGANVLT 171

QY 129 PEALGLHLQALTASKVQVSLYKSKSDLNKICYKSGVPLIENGMIEMIEKLPFCVILTP 188

Db 172 TEALLQHLDSALQASRVHVVMYNNQWKLHLCYKSGELITETGYMDQIIEVLYPCLLIITP 231

QY 189 LDCFWEGAKLGGGSAIYPGRPDIOVNTLDPQLLEELGPF-ASLEGPRELLDQAQVQAY 247

Db 232 LDCFWEGAKLQSGTAYLLGKPLPPLRWTFNDFLEFLEELKKINYYQVDSWEEMLNKAEVGHGY 291

QY 248 VGRPCLHPDDLHCPSPAPNHSRQAPNVAHELSCGCHGFHKKFMHMOBELLLGQWARDPQ 307

Db 292 MDREPCLNADPCPCATAPNKNSTKPLDMALVLANGCHGLSRKYMHWQEEILVGVTKVNST 351

QY 308 GELLRAEALQSTFLMSPROLYEHFRG-DYQTHDIGHSEEQASTVLOAWORRFVQLAQEA 366

Db 352 GKLVSAHALQTMFLTPKQMEYHFKEGYEVSH-INWNEDKAAAILAEAWORTVEVHHQS 410

QY 367 LPENASQOIHAFFSSTLDDILHAFSVSAARVVGGVLLMLAYACVMTLWRDCAOSQSVG 426

Db 411 VAQNSTQKVLSTFTTLLDDILKSFSDSVIRVASGYLLMLAYACLTLMLRDCRSQGAVG 470

QY 427 LAGVLLVALAVASGLGLCALLGITFNAATQVLPFLALGIGVDVDFLLAHAFTEALPG-- 484

Db 471 LAGVLLVALSVAAGLGLCSLIGISFNAATQVLPFLALGVGDDVFLAHAFSETGQNK 530

QY 485 TPQERMGECLQRTGTSVLTSSINNMAAFUMLALVPIPALRAFSLQAAIIVGCTTFVAVML 544

Db 531 IPFEDRTGECLKRTGASVALTSISNTAFPMALIPALRAFSLQAAVVVVFNFAMVLL 590

QY 545 VFPAILSLDLRRRCORLDVLCFSSPCSAQVLIQLPQELGD-----GTVPVGIH-- 595

Db 591 IFFAILSMDDYRRDRRLDFCCFTSPCVSRVQVEPQAYTDHNTRYSPPPPYSHSF 650

QY 596 -----LTATVOAFTHCEASSQHVVTILPPQAHVPPP----SDPLGSELFSPGGSTRD 644

Db 651 AHETOITMSTVQLRTEYDPHTHVYTTAEPRSEISVQPVTVTQDTLSCQSPSTSTRD 710

QY 645 LLQGEETROKAAACKSLPCARWNLAHFARYQFAPLLLOSHAKAIVLVFGALLGLSLYGA 704

Db 711 LLSQFSDS--SLHCLPEPCTKWLSSFAEKHYAPFLKPKAKVVVIFLFLGLLGSUYGT 768

QY 705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYSLSYELVALVTCGGPDYHAHQRAFLDHFORS 764

Db 769 TRVRDGLDLDIVPRETRYDFIAAQKYFSFTNMYITVOKA-DYPMIQLHLLDHLRSFS 827

QY 765 SLKAVLPPPAPATQAPRTWLYHYRNWLOGIAQAFQDDWASGRITRHSYENGSEDEGALAYKL 824

Db 828 NVKVMLEENKQLPKMWLHYFRDMLQGLQDAFDSWETGKIMNNYKNGSDDGVLAYAKLL 887

QY 825 IQGDAQEPLDPSQLTRKLVLDREGLIPPELPMGLTVWVSSDPLGLAASQANFYPPPPPE 884

Db 888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWYNSNDPVAAYASQANIRHPRE 947

QY 885 WLHDKVDYTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADFEALEGARAAACAGAGVH 943

Db 948 WVDHKADYMPETRLRIPAAEPIEYAOFPFYVNGRLRTSDFEALEKVRTICSNYTSUGLS 1007

QY 944 AYPGSPFLFWEQYGLRRCFLLAVCILLVCTFLVCALLLNPNWTAGLIYLVLAMTVEL 1003

Db 1008 SYNGYFPLFWEQYIGLRHWLLLFISVLACTFLVCVAVFLNPNWTAGLIYVVLALMTVEL 1067

QY 1004 FGIMGFLGKLSAIPVVILVASVIGVEFTVHVVALGFLTTQGSRNLRRAHALEHTFAPVT 1063

Db 1068 FGMMGLIGKLSAVPVVILLIASVIGVEFTVHVVALAFLTAIGDKNRRRAVLALEHMFAPVL 1127

QY 1064 DGAISTLIGLLMAGSHDFIVRYEFAALVTLTLGLLHGLVLLPVLSSLILGPPPEVI-- 1121

Db 1128 DGAVSTLGLVIMLAGSEDFIVRYFAVLAAILTLILVINGLVLVLLPVLSSFPGPYEVSFA 1187

QY 1122 ----QMKESPE-----ILSP-----APQGG 1139

Db 1188 NGLNRLPTSPPEPPSVVRFAMPFGHTGSSDSDSEYSSQTTVSGLSBELRHYEQGA 1247

QY 1140 G-----LRWG-----ASSLSQSFAR 1155

Db 1248 GGAHQVIVEATENPVFAHSTVVHPSRHHPPSNRQPHLDGSLPPGRRDPP 1307

QY 1308 REGMLPPLVYPRRDAFEISTEGHSGPSNRARWGRGARSHNPNRNPASTAMGSSVPGYQCP 1367

Db 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176

QY 1368 ITTVTASASVTVAHPHPPVPGGRNP 1393

RESULT 13

US-08-954-701A-19

; Sequence 19, Application US/08954701A

; Patent No. 6610507

; GENERAL INFORMATION:

; APPLICANT: SCOTT, MATHEW P

; APPLICANT: GOODRICH, LISA V

; APPLICANT: JOHNSON, RONALD L

; TITLE OF INVENTION: Patched Genes and their Use

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley, Hoag & Eliot

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/954,701A

; FILING DATE: 20-OCT-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36709

; REFERENCE/DOCKET NUMBER: SUV-003.08

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1447 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-954-701A-19

Query Match 53.4%; Score 3348; DB 4; Length 1447;
 Best Local Similarity 49.9%; Pred. No. 1.7e-314;
 Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPARTAAPQILAGSL---KAPLWLRAYFQGLLFSGLCGIQRHCGKVLFLGLLAFGA 68
 DB 53 PSYC-DAAFALQISKKATGRKAPLWLRKAFQRLFLKLCYIQKCGKFLVVGLLIFGA 111
 QY 69 LAIGLRMAIETNLEQLWVEGSRVSOELHYTKEKLEGEAAAYTSQMLIQARQEGENILT 128
 DB 112 FAYGLKAANLETNVEELWVEGSRVRELNYTRQKIGEEAMFNPLQMIQTPKEGANVLT 171
 QY 129 PEALGHLOALTASKVOVSLYKSGDNLNKICVKSGVPLLENGMIENMIEKLEPCVLTLP 198
 DB 172 TEALLQHLDSALQASRVHVHTYRQWKLKHLCKYSGELITETGYMDQIIEYLYPCLIITP 231
 QY 189 LDCFWGAKLQGSAYLPGRPDIQWNTLDPQLEELGPPF-ASLEGFRELDDKAQVQYAY 247
 DB 232 LDCFWGAKLQSGTAYLLGKPLPLRWTFNFDPLEFLEELKKNYQVDSWEEMLNKAEVGHY 291
 QY 248 VGRPCPLHDDLHCPGAPNHSQAQPNVAHELGGCHGFGSKPMHWQEBELLGLGMARDPQ 307
 DB 292 MDRPCPLNPADPCFAPAPNKNSTKPLDMALVNLGGCHGLSRKYNHWQEEILVIGTGVKNST 351
 QY 308 GELLRAEALQSTFLLMSPROLYEYHFRG-DYOTHDIGWSEQAQSTVLQAWORRRFVOLAQA 366
 DB 352 GKLVSANALQTMQLMTPKQMYEHFKGYEVSH-INNWEDKAAILEAWORTVEVHVQS 410
 QY 367 LPENASQIHAFSSTLDDIILHAFSEVSAARVGVGYLLMLAYACVTMLRWDCAQSGSVG 426

DB 411 VAQNSTQKVLSTFTTTLLDDILKSEDSVSVIRVAGSYLLMLAYACLTMLRWDCKSQGAVG 470
 QY 427 LAGVLLVALAVASGLGICALLGHTFNAAATTVLPFLFALGIGVDDVFLLAHAFTALPG-- 484
 DB 471 LAGVLLVALSVAAGLGLCSLIGISFNAAATTVLPFLFALGIGVDDVFLLAHAFTALPG-- 530
 QY 485 TPLQERMGECLORTGTSVWVLTISNNMAAFMAALVPIPALRAFSQAIAIVVGCTFVAVML 544
 DB 531 IPFEDRTGECLEKRTGASVALTSISNVTAFFMAALIPALRAFSQAIAIVVGCTFVAVML 590
 QY 545 VFPAILSLDLRRHRCORLDVLCFSPSCSAQVLIQLPOELGD-----GTPVPGIAH-- 595
 DB 591 IFFAILSMDDLYRRDRLDIFCCFTSPCVSRVQVEEQAYTTHDNTRYSPPPYSSHSF 650
 QY 596 -----LTATVQAFTHCEASSQHVVTILPFOAHLVPPP-----SDPLGSELFSPGSGTRD 644
 DB 651 AHETQITMQSTVQLRTEYDPHTHYTTAEPRSEISVQPVTVTQDTLSCQSPSTSTTRD 710
 QY 645 LLGOEETROKAAKSLPCARWNLAHFARYQFAPLLLOSHAKAIVLVLFGALLGLSLYGA 704
 DB 711 LLSQFSDS--SLHCLPEPPCTKWLSSFAEKHYAPFLKPKAKVWVIFLFLGLLGLSYLGT 768
 QY 705 TLVODGLALTVDVVRGTKEHAFLSAQLRYESLYEVALVTOGGEDYAHQSORALFDLHORFS 764
 DB 769 TRVEDGLDLTDIVPRETREVDFATAQPKYFSFVNMVIVTQKA-DYPNIQHLLYDLHRSFS 827
 QY 765 SLKAVLPPPTAQPTWMLHYRNWLGIOQAAPQODWASGRITRHSYRNGSESDGALAYKLL 824
 DB 828 NVKYVMLEENKQLPKWMLHYFRDLWGLQDAFSDMETGKIMPNNYKNGSDDGVLAYKLL 887
 QY 825 IOTGDAQEPLDLSQITRKLVDREGLIPPELFYWGTLVWVSSDPLGLAASQAQNPYPPE 884
 DB 888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFVIYLTAWVSNDFVAVAAQAIRPPE 947
 QY 885 WLHDKYDITGE-NLRIPPAQPLEFAQPPFLRLGLQKTADFEVALEGAARACAAGQAGVH 943
 DB 948 WYHDKADYMPETRLRIPAEPIEYQAPFFVYNGLRDTSDFEVALEKVTTCNSYTSGLS 1007
 QY 944 AYPGSPFFLWEOYGLRRCFLAVCILLVCTFLVALLLNPNWTAGLIIVLVLAMMTVEL 1003
 DB 1008 SYPNGYPLFWEOYIGLRHMLLLFISVLACTFLVCAVFLNPNWTAGLIIVMLALMTVEL 1067
 QY 1004 FGLWGLGILKLSAIPVVLVAVSGIGVEFTVHVALGFLTTQGSNLRRAHALEHTPAVPT 1063
 DB 1068 FGMMGIIGIKLSAVPVVILIASVIGVFTVHVALAFLTAIGDKNRRAVLAHEMFAPVL 1127
 QY 1064 DGAISTLLGLLGLAGSHFDIVRYFFAALTVLLGLLHGLVLLPVLLSLTILGPPPEVI-- 1121
 DB 1128 DGAVSTLLGLVLMLAGSEFFDIVRYFFAVLAILIILGVINGLVLVLLSFFGYPPEVSPA 1187
 QY 1122 -----QWYKESPE-----ILSPP-----APQGG 1139
 DB 1188 NGLNRLPTSPPEPPSVVRFPAMPFGHTHSGSDSDSEYSSQTTVSGLSGLSELRHYEQQA 1247
 QY 1140 G----- 1140
 DB 1248 GGAHVIVTEATNPVFAHSTVHVHPSRHHPNPNRQOQPHLDGSLPPGQGGQPPRRDPP 1307
 QY 1141 -----LRWG-----ASSLSQSFAR 1155
 DB 1308 REGWLPLYRPRDAFEISTEGHSGFSNRARWGPRGARSHNPNPASTAMGSSVPGYQCP 1367
 QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
 DB 1368 ITTVTASVTVAVHPPVPVPGGRNP 1393

RESULT 14

PCT-US95-13233-19

; Sequence 19, Application PC/TUS9513233

; GENERAL INFORMATION:

; APPLICANT: THE BOARD OF TRUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY

; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13233
 ; FILING DATE: 06-OCT-1990
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1447 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-13233-19

Query Match 53.4%; Score 3348; DB 5; Length 1447;
 Best Local Similarity 49.9%; Pred. No. 1.7e-314;
 Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSTPTPARTAAPQILAGSL---KAPLMIRAYFQGLFLSLGCGTQRHCGKVLFLGLIAFGA 68
 DB 53 PSYC-DAAFALQTSKGTAKRKAFLMLRAKFORLLFLKGCYTKNCKGKFLVWGLLIFGA 111
 QY 69 LAIGLRMAIETLEQLWVEGSRVSOELHYTEKLEGEAAAYTSOMLIQTARAGEENILT 128
 DB 112 FAVGLKAANLETVBEELWVEGSRVSELNYTRQKTIGEEAMFNPQMIQTPKEEGANVLT 171
 QY 129 PEALGLHLOALTASKVQVSLYKSWDLNKCICKYSGVPLTJENGMIEMIEKLPFCVILTLP 188
 DB 172 TEALLQHLDSALQASRVHVVMYRNQWKLHLCYKSGELITETGYMDQIIEYLXPCLLIITP 231
 QY 189 LDCFWEAGAKLQGSAYLPGRPDPTQWNLDPQLLELGLPF-ASLEGFRELLDKAQVQGYAY 247
 DB 232 LDCFWEAGAKLQGSAYLPGRPDPTQWNLDPQLLELGLPF-ASLEGFRELLDKAQVQGYAY 291
 QY 248 VGRPCLHPDPLHCPSPANHNSRQAPNAHVELSGCHGFSKEMHCEELLLGSMARDPQ 307
 DB 292 MDRPCLNPADPCFATAPNKNSTKPLDMALVNLGCGHGLSRKYMHQBELIVGGTVKNST 351
 QY 308 GELLRAEALQSTFLMSPRLQYEHFRG-DYQTHDIGWSEEQASTVQLQAWQRRFVQLAQEA 366
 DB 352 GKLVSAHALQTMFQMTKQMYEHFKGYEVVSH-INWNEKAAALILEAQRTYVEVHQH 410
 QY 367 LPENASQOIHAFSTLDDILHAFSEVSAARVVGYYLLMAYACVTMLRWDCQSQSGV 426
 DB 411 VAQNSTQKVLFSFTTTTLLDILKFSVSVTRVSAVGLLMLAYACLTMLRWDCSKSQGAVG 470
 QY 427 LAGVLLVALAVASIGICALLGTEENAAATTOVLPELAGIGVDDVFLLAHAFTEALPG-- 484
 DB 471 LAGVLLVALVSAAGLGLSIGISFNAAATTOVLPELAGIGVDDVFLLAHAFSETGONKR 530
 QY 485 TPLQERMGECLQRTGTSVLTSTNNMAAFMLAALVPIPALRAFSLQAAIIVVGCTFVAVML 544
 DB 531 IPEDRTGECLRTGASVALTSISNVTAFMAALIPIPALRAFSLQAAVAVVVFNAFVLL 590

QY 545 VFPAILSLDLRRRHRCORLDVLCFSSPSCSAQVITQILPOELGD-----GTVPVGIAM-- 595
 DB 591 IFPAILSMDLYRRDRRLDIFCCFTSPCVSRVITQVEFQAYTDTHTDNTRYSPPPPYSSHFS 650
 QY 596 -----LTATVCAFTHCRASSQHVVTILPQOAHVPPP-----SDPLGSLFSPGGSTRD 644
 DB 651 AHETQITMQSTVQURTEYDTHVYTTAEPRESEISVQPVTVTQDTLSCSPSESTSTRD 710
 QY 645 LLQGEETRQKAAKSLPCARMNLAHFARYQFAPLLIQLSHAKAIVLIFGALLGLSLYGA 704
 DB 711 LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLLPKPAKVIVIFLFLGLLGVSLYGT 768
 QY 705 TLVQDGLALDVTVPRTGKEHAFSLAQRYFSLYEVALVTQGGFDYAHQSRALEDLHORFS 764
 DB 769 TRVRDGLDLTDIVPRETREYDFIAAQKFYSFFNMVITQKA-DYPNIQHLLDLHRSFS 827
 QY 765 SLKAVLPPPATOAPRTMLHYRNWLOGIOAAFDODWASGRITRHSYRNGSEDCALAYKLL 824
 DB 828 NVKYVMLEENKQLPKWMLHYFRDMLQLODAFSDMETGKIMPNYKNGSDGGLAYKLL 887
 QY 825 IQTGAQEPDLFDSQLTTRKLVDRGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPE 884
 DB 888 VQTGSRDKPIDISQLTQKRLVDADGIINPSAFYILTAWVSNDPVAYAAQANIRPURPE 947
 QY 885 WLHDKYDTTGE-NLRTPPAQPLEFAQPPFLLRLGLOKTADFEVAIEGARAACAAGQGVH 943
 DB 948 WHDKADYMPETRLRIIPAAEPIEYQAQFPFYNLGRLDTSDFEAEIKVRTTICSNYTSGLS 1007
 QY 944 AYPGSGPFLFWEQYGLRRCFLILAVCILLVCTLCVLCALLLNPTWAGLIVLVLAMTVEL 1003
 DB 1008 SYENGYPFLFWEQYIGLRWLLLPISVVLACTELVCVAVLLNPTWAGIIVVVLAMTVEL 1067
 QY 1004 FGIMFGLIKLSAIPVILVASVIGVFTVHVVALGFLTQGSRNLRRAHALEHTFAPVT 1063
 DB 1068 FGMWGLIGIKLSAVPVILLIASVIGVFTVHVVALGFLTQGSRNLRRAHALEHTFAPVT 1127
 QY 1064 DGAISTLLGLLMLAGSHDFIVRYFFAALTTLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
 DB 1128 DGAISTLLGLVLMAGSEDFIVRYFFAVALAILTLGLVNLGLVLLPVLLSFFGYPYEVSPA 1187
 QY 1122 ----QMYKESPE-----ILSP-----APOGG 1139
 DB 1188 NGLNRLTPSPPEPPSVVRFAFMPGHTHSGSDSDSEYSSQTTVSGLSELRHYEAQOGA 1247
 QY 1140 G-----LRWG----- 1140
 DB 1248 GGPAAQVIVEATENPVFAHSTVVHPESRHHPPSNPRQOQPHLDGSLPPGQOQPRDPP 1307
 QY 1141 -----LRWG-----ASSLSPOSFAR 1155
 DB 1308 REGMLPPLXPRRDAFEISTEGHSGPSNRARWGPGRGSHNPRNPASTAMGSSVPGYCOP 1367
 QY 1156 VTT-----SMTVAIHPPPLPGAVIHP 1176
 DB 1368 ITTVTASAVTVAVHPPPPVPGGRNP 1393

RESULT 15

US-08-540-406-10
 ; Sequence 10, Application US/08540406
 ; Patent No. 5837538
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V
 ; APPLICANT: JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA

; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 06-OCT-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: 860190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1434 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-540-406-10

Query Match 53.2%; Score 3337; DB 2; Length 1434;

Best Local Similarity 53.1%; Pred. No. 1.9e-313;

Matches 672; Conservative 206; Mismatches 339; Indels 78; Gaps 20;

Qy	3	RSPLREL--PPSTTPARTAAPOILAGSL--KAPLWRAYPFOGLFSLGCGFORHCGK	57
Db	28	RAPDRYLHRPSYC--DAAFALQISGKATGRKAPLWRAKFORLLFKLGCYIQKNCCK	86
Qy	58	VLFGLAFALALGLRMAIETNLEQLWVEVSGRVSQELHYTKELGEBEAAAYTSQMLIQ	117
Db	87	FLVVGLLIFGAFVAGLKAANLEINVELWVEVSGRVSRELNYTRQKIGEEAMFNPQLMIQ	146
Qy	118	TARQEGENIITPEALGHQLQAALTASKVQVSLYKSDNLNKICYKSGVPLIENGMIEMWI	177
Db	147	TPKEEGANVLITTEALLQHLDSALQASRVHYVMYNRQWKLEHLCYKSGELITETGYMDQII	206
Qy	178	EKLFPVCVILTPLCFWEKALQGGSAYLPGRPDIQWNLDPQELLEELGPF--ASLEGFRE	236
Db	207	EYLYPCLIIITPLCFWEKALQGGSAYLPGRPDIQWNLDPQELLEELGPF--ASLEGFRE	266
Qy	237	LLDKAQVQAYGRPCLPDPLHCPPSAPNHSGRQAPNVAHELSCGCHGFSHKPMHWQEE	296
Db	267	MLNKAEVGHGMDRCPCLNPADPCPATAPNKNSTKPLDVALVNLGGCQGLSRKYMHWQEE	326
Qy	297	LLGGWARDPQRELLRAEALQSTFLMSPRQLYEHFEG--DYQTHDIDGWSBEQASTVLQAW	355
Db	327	LIVGGTVKNATGKLVSAAHALQTMFQMLPKOMYEHFEGDYVSH--INWNEDRAAAILLEAW	385
Qy	356	QRFRVLOALPENASQIIFATSTTDLIDILHAFSEVSAARVVGVGYLLMLAYACTVTLR	415
Db	386	QRTYVEVHQSVAPNSTQKVLPTTTITLIDILKSFSDSVIRVASGYLLMLAYACTVTLR	445
Qy	416	WDCAQSGSVGLAGVLLVALAVASGLCALLGITFNAATQVLPFLALGIGVDDVVELLA	475
Db	446	WDCSKSQAGVLAGVLLVALSVAAGLCLSLIGISFNAATQVLPFLALGIGVDDVVELLA	505
Qy	476	HAFTEALPG--TPIQERMGECLORTGFSVVLTSINWAAFLMAALVPIPALRAFSLOAAI	533
Db	506	HAFSETQNKRIEFTQREGLKRTGASVALTSISNVTAFFMAALVPIPALRAFSLOAAI	565
Qy	534	VVGCTFVAVMLVFALISLDRRHQRDLVCCFSSPCSAQVITQILPQELGD-----	586
Db	566	VVVFNFAMVLLIPIALISMDLYRREDRLDI FCCFTSPCVSRVIOVEPQAYTEPHSNTRY	625
Qy	587	GTVPVGTIAH-----LTATVQAFTHCEASSQHVVTILPQAHLVPPP-----SDPLGS	633

Search completed: November 22, 2004, 07:58:45

Job time : 34 secs

Db	626	SPPPYTSHSFAHETHITMQSTYQQLRTEYDPHTHYVYTTAEPRSEISVQPVTVTQDNLSC	685
Qy	634	ELFSPGGSTRDILLQEBETROKAAKSLPCARWNLAHFARYQFAPILLQSHAKAIVLVLF	693
Db	686	QSPSTSSSTRDILLQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVYVILF	743
Qy	694	GALLGLSLYGATLVQDGLALTDDVPRGTGKEHAFSLAQLRVFSLYEVALVTQGGDFYAHSQ	753
Db	744	LGLLGLSLYGTTRVRDGLDITDIPRETREYDFIAQFKFYSFNMVIVTQKA--DYNIQ	802
Qy	754	RALFDLHQREFSSLKAVLPFPATQAPRTWLYHYRNWLOGIQAAFDQDQDQDQDQDQDQDQDQ	813
Db	803	HLLYDLHKSPSNVYVMLEENKQLPQWLHYFRDLQGLQDAFSDWETCRIMPNNYKNG	862
Qy	814	SESGALAYKLLIQTGDAQEPDLSQLTTRKLVOREGLIPPELFWMGITVWVSSDPLGLAA	873
Db	863	SDGVLAYKLLVQTSRDKPIDISQLTQKQLVDADGIINFSAFYIYLTAWVSNPDVAYAA	922
Qy	874	SQANFYPPPEWLHDKYDTTGE--NLRIPPAQPLEFAQFPFLRLGLOKTADEFVEAIEGARA	932
Db	923	SQANIRHPREWHDKADYMPETRLRIPAAEPYEAQFPFLNGLRDTSDFVEALEKVRV	982
Qy	933	ACAEAGQAGVHAYPSSGPFLEWQYLGRLRCFLAVCILLVCTFLVCAALLLNPTWAGLI	992
Db	983	ICNNYTSGLSSYPNGYPPFLWQYISLRHLLLSISVWLACTFLVCAVLLNPWTAGII	1042
Qy	993	VIVLMMTVBELFGIMGLGKLSAIPVILVASGIGVEFTHVVALGFLTQGSNRURAA	1052
Db	1043	VVVALMTVELFGMGLGKLSAIPVILVASGIGVEFTHVVALGFLTQGSNRURAA	1102
Qy	1053	HALEHTPAPYTDGAISTLLGLLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLLS	1112
Db	1103	LALEHTPAPYTDGAISTLLGLLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLLS	1162
Qy	1113	ILGPPPEVI-----QMYKESPEILSPP-----APQGGGLRWGASSLSQSFARVTTTS--	1159
Db	1163	FFGCPCEVSPANGNLRLPTSPB--PPSVVREAVPPGHTNNGSDSDSDSEVSSQTTVSGI	1220
Qy	1160	-----MTVALHPPLPGAYIHP--APDEPPKSPAA---TSSGNLS	1194
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Qy	1195	SRGPG 1199	
Db	1281	---PG 1282	

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 08:02:26 ; Search time 155 Seconds
(without alignments)
5516.639 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues
Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
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6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6272	100.0	4030	US-09-293-505-1	Sequence 1, Appli
2	6272	100.0	4030	US-09-060-939A-1	Sequence 1, Appli
3	6248	99.6	4391	US-09-207-857-1	Sequence 1, Appli
4	6248	99.6	4391	US-09-309-280A-1	Sequence 1, Appli
5	3955	63.1	4004	US-09-293-505-8	Sequence 8, Appli
6	3955	63.1	4004	US-09-060-939A-8	Sequence 8, Appli
7	3387	54.0	2082	US-09-293-505-9	Sequence 9, Appli
8	3387	54.0	2082	US-09-060-939A-9	Sequence 9, Appli
9	3349	53.4	5288	US-08-540-406-18	Sequence 18, Appl
10	3349	53.4	5288	US-08-656-055-18	Sequence 18, Appl
11	3349	53.4	5288	US-08-954-668-18	Sequence 18, Appl
12	3349	53.4	5288	US-08-918-658-18	Sequence 18, Appl

13	3349	53.4	5288	4	US-09-724-631-18	Sequence 18, Appl
14	3349	53.4	5288	4	US-08-954-701A-18	Sequence 18, Appl
15	3349	53.4	5288	5	PCT-US95-13233-18	Sequence 3, Appli
16	3337	53.2	5187	2	US-08-540-406-3	Sequence 3, Appli
17	3337	53.2	5187	2	US-08-540-406-3	Sequence 9, Appli
18	3337	53.2	5187	3	US-08-556-055-3	Sequence 3, Appli
19	3337	53.2	5187	3	US-08-556-055-9	Sequence 9, Appli
20	3337	53.2	5187	3	US-08-954-668-3	Sequence 3, Appli
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30	3336	53.2	6568	4	US-08-857-636-1	Sequence 1, Appli
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33	1972.5	31.4	3900	3	US-08-460-900C-42	Sequence 42, Appl
34	1972.5	31.4	3900	3	US-08-674-509B-42	Sequence 42, Appl
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37	1972.5	31.4	3900	4	US-09-639-695-42	Sequence 42, Appl
38	1972.5	31.4	3900	4	US-09-448-188-42	Sequence 42, Appl
39	1972.5	31.4	3900	4	US-08-954-128-42	Sequence 42, Appl
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41	1972.5	31.4	3900	4	US-09-736-476-42	Sequence 42, Appl
42	1956	31.2	4434	2	US-08-540-406-5	Sequence 5, Appli
43	1956	31.2	4434	3	US-08-656-055-5	Sequence 5, Appli
44	1956	31.2	4434	3	US-08-954-668-5	Sequence 5, Appli
45	1956	31.2	4434	4	US-08-918-658-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-293-505-1
; Sequence 1, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 1
; LENGTH: 4030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-293-505-1

Alignment Scores:
Pred. No.: 0
Score: 6272.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 4030
Matches: 1203
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-990-046-2 (1-1203) x US-09-293-505-1 (1-4030)

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QY	21	AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe	40

Db 293 GCAGCACCAGATCCTAGCTGGAGCCTGAAGGCTCCACTCTGGCTTCTGTCTTACTTC 352
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41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyIysValLeuPhe 60
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81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
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121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
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 QY 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
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 DB 3293 ATCCTTGTGGCTCTGTAGGCAATGGCGTTAGTTCACAGTCCACGCTCGGCTCTGGCTTC 3352
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 QY 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
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 QY 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGly 1140

DB 3593 ATACAGATGTACAGAAAGCCAGAGATCTTGAGTCCACCTCCAGAGGAGCGGG 3652
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 DB 3653 CTTAGTGGGGGATCT 3712
 QY 1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
 DB 3713 ACCGTGGCATCACCCACCCCTCTGCTGGTGGCTTACATCATCATCATCATCATCAT 3772
 QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
 DB 3773 CCCCCTGTGGTCT 3832
 QY 1201 AlaThrGly 1203
 DB 3833 GCCACTGGG 3841
 RESULT 2
 US-09-060-939A-1
 ; Sequence 1, Application US/09060939A
 ; Patent No. 6709838
 ; GENERAL INFORMATION:
 ; APPLICANT: Frederic de Sauvage, David A. Carpenter
 ; TITLE OF INVENTION: Patched-2
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,939A
 ; FILING DATE: 15-Apr-1998
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39,044
 ; REFERENCE/DOCKET NUMBER: P1405
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4030 base pairs
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; US-09-060-939A-1
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 Score: 6272.00 Matches: 1203
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
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 QY 1 MetThrArgSerProProLeuArgGluLeuProSerTyrThrProProAlaArgThr 20
 DB 233 ATGACTCGATCGCGCCCTCAGAGAGCTGCCCCGAGTTACACACCCCGAGCTCGAAC 292
 QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40

|||||
293 GCAGACCCAGATCCTAGCTGGAGCTGAAGGCTCCACTCTGGCTTCGTACTTTC 352
QY
41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db
353 CAGGGCCCTGCTCTCTCTCTGGGATGCGGGATCCAGAGACATTTGGCAAGTGTCTCTTT 412
QY
61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db
413 CTGGGACTGTGGCCCTTTGGGGCCCTGGCATTAGGFTCCGATGGCCATTATTGAGACA 472
QY
81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db
473 AACTTGGACAGACTCTGGGTAGAGTGGCAGCCGGGTGAGCCAGAGCTGCATTACACC 532
QY
101 LysGluLysLeuGlyGluGluAlaIaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db
533 AAGGGAAGCTGGGGAGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC 592
QY
121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
Db
593 CAGGAGGAGAGACATCTCTCACCCGAGAGCACTTGGGCTCCACCTCCAGGAGGCCCTC 652
QY
141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db
653 ACTGCCAGTAAGTCCCAAGTATCACTCTATGGGAAGTCTCTGGGATTTGAACAAAATCTGC 712
QY
161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db
713 TACAAGTCAAGGATTCCTCTTATTTGAAAATGGAATGATTTGAGTGGATGATTGAGAAGCTG 772
QY
181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db
773 TTTCCGTGGTGAATCTCACCCCTCTGACTGCTTCTGGAGGGAGCCAACTCCAAAGGG 832
QY
201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db
833 GGCTCCGCTACTCTGCCCGCGCCCGGATATCCAGTGAGCCACCTGGATCCAGAGCAG 892
QY
221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db
893 CTGCTGGAGGAGTGGGTCCCTTTGCTCTCCCTTTAGGGCTTCCGGGAGCTGTAGACAAG 952
QY
241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
Db
953 GCACAGTGGCCAGGCCCTACGTGGGGCGGCCCTGTCACCTGATCACCCTCCACTGC 1012
QY
261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db
1013 CCACCTAGTGCCCCCAACCATCACAGCAGGAGCTCCCAATGTGGCTCACGAGCTGAGT 1072
QY
281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
Db
1073 GGGGGTGCATGGCTTCTCCACAAATTCATGCATGGCAGAGGAAATTTGCTGTGGGA 1132
QY
301 GlyMetAlaArgAspProGlnGlyGluLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db
1133 GGCAATGCCAGAGACCCCAAGAGAGAGCTGTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192
QY
321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db
1193 TTGCTGATGAGTCCCCCGCCAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 1252
QY
341 IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal 360
Db
1253 ATTGGCTGGAGTGAGAGCAGGCCACAGCAGTGCTACAAGCCCTGAGCGGGCTTTGTG 1312
QY
361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db
1313 CAGCTGGCCCCAGAGGCCCTGCTGAGACGCTTCCAGCAGATCCATGCCTTCTCTCTCC 1372
QY
381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400

1373 ACCACCTGGATGACATCCTGCATCGCTTCTCTGAAGTCAGTGTGCCCGCTGTGGTGGGA 1432
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401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
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1433 GGCTATATGCTCATCTGGCCCTATGCTGTGTGACCATGCTCGGTGGGACTGCGGCCAG 1492
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421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
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1493 TCCAGAGGTTCCTGGGCCCTTCCCGGGGTACTGCTGTGTGGCCCTGGCGGTGGCCCTCAGGC 1552
QY
441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db
1553 CTTGGCTCTGTGCCCTGTCTGGCATCACCTTCAATGCTGCCACTACCCAGGTGTGCTCT 1612
QY
461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db
1613 TTCTTGGCTCTGGGAATCGGCGTGTGATGACGTATTCTCTCTGGCGATCCCTTTCACAGAG 1672
QY
481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db
1673 GCTCTGCTGGCACCCCTCTCCAGGAGCGCATGGCGAGTGTCTGCAGCGACGCGGCACC 1732
QY
501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db
1733 AGTGTGCTACTCACATCCATCAACAACATGGCGCGCTTCTCTCATGGCTGCCCTCGTCC 1792
QY
521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db
1793 ATCCCTGGCCTCGAGCCCTTCTCCCTACAGGGCGCATAGTGGTGGCTGGACCTTTGTA 1852
QY
541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln 560
Db
1853 GCGGTGATGCTTGTCTTCCCGCCATCTCAGCCTGGACCTACGGGGCGGCCACTGCCAG 1912
QY
561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db
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Db
1973 CCCCAGGAGCTGGGGAGCGGACATTACAGTGGGCAATTTGCCCACTCTACTGCCAGATT 2032
QY
601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
Db
2033 CAGACCTTTACCACATGTGTGAAGCCAGCAGCATGTGTGTCACCATCTCTGCTCCCCAA 2092
QY
621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db
2093 GCCCACCTGGTGCCTCCACCTTCTGACCACCTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
QY
641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db
2153 TCCACACGGGACCTTCTAGCCAGGAGGAGGAGACAAGGCAAGGACGACCTGCCAAGTCC 2212
QY
661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db
2213 CTGGCCTGTGCCCGCTGGAACTCTGCCCATTTCCGCCCTATCAGTTTCCCGCTGTGCTG 2272
QY
681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db
2273 CTCCAGTCAATGCCAAGGCCATCGTGTGCTCTTTGGTGCTCTTCTGGGCCCTGAGC 2332
QY
701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db
2333 CTCTACGGAGCCACCTTGTGTGAGAGCGCCCTGGCCCTGACGGATGTGTGCTCGGGGC 2392
QY
721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db
2393 ACCAAGGAGCATGCTCTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC 2452
QY
741 LeuValThrGlnGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db
2453 CTGGTGACCCAGGCTTTGACTACGCCCATTTCCAAACGCGCCCTCTTTGATCTGAC 2512

QY 761 GluArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr 780
Db 2513 CAGCGCTTCAGTCCCTCAAGGGCTGCTGCCGCCACCGCCACCCAGGACCCCGCACC 2572
QY 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyLeuAlaPheAspGlnAspTrp 800
Db 2573 TGGCTGCACTATTACCGCAACTGGCTACAGGAATCCAGAGCTGCCCTTGACAGGACTGG 2632
QY 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2633 GCTTCTGGGGCGCATCACCCGCCACTCGTACCGAATGGCTCTCAGGATGGGGCCCTGGCC 2692
QY 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2693 TACAGCTGCTCATCCAGACTGGAGAGCGCCAGAGCCTCTGGATTTCAGCCAGCTGACC 2752
QY 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2753 ACAAGGAAGCTGGTGACAGAGAGGACTGATTCCACCCGAGCTCTTACATGGGGCTG 2812
QY 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2813 ACCGTGGGTGAGCATGCCCTCCCTGGGTCTGGCAGCCTTCACAGGCCAACTTCTACCCC 2872
QY 881 ProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2873 CCACCTCTCGAATGGCTGCAGCAATACGACACCCAGGGAGAACCTTCGCATCCCG 2932
QY 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2933 CCAGCTCAGCCCTGGAGTTGGCCAGTTCCCTCTCTGCTGGTGGCCTCCAGAGACT 2992
QY 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 2993 GCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGCCGGCCAGGCT 3052
QY 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db 3053 GGGGTGCACGCTTACCCAGCGCTCCCCCTCTCTCTGGGAAACAGTATCTGGGCGCTG 3112
QY 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 3113 CGGCGCTGCTTCTGCTGGCGCTGCTGCATCTCTGCTGGTGTGCACTTCTGCTGTGCT 3172
QY 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db 3173 CTGCTGCTCTCAACCCCTGGACCGGTGGCTCATAGTCTGCTGCGCATGATGACA 3232
QY 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db 3233 GTGGAACTCTTTGGTATCATGGGTTTCTGGGCATCAAGCTGAGTGCCATCCCGGTGGT 3292
QY 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db 3293 ATCCCTTGTGGCTCTGTAGGCATTGGCGTTGAGTTACAGTCCAGTGGCTCTGGGCTTC 3352
QY 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3353 CTGACCAACCCAGGGCAGCGGAACTTGGGGCGGCCCATGCCCTTGGACACACATTTGCC 3412
QY 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyIleLysLeuMetLeuAlaGlySerHis 1080
Db 3413 CCCGTGACCGATGGGGCCATCTCCACATGCTGGGTCTGCTCATGCTGCTGGTTCGCCAC 3472
QY 1081 PheAspPheIleValArgTyrPhePheAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db 3473 TTTGACTTCATTGTAAGGTACTTCTTTCGGCGCTGACAGTGTCTACGCTCTCTGGGCTTC 3532
QY 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
Db 3533 CTCCATGGACTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3592

QY 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGly 1140
Db 3593 ATACAGATGTACAAGGAAGCCAGAGATCCTGAGTCCACAGCTCCACAGGAGGCGGG 3652
QY 1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db 3653 CTTAGGTGGGGGCATCTCTCTCCCTGCCAGAGCTTTGCCAGAGTACTACCTCCATG 3712
QY 1161 ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db 3713 ACCGTGGCATCCACCCACCCCTGCTGGTGCTACATCCATCCAGCCCTGATGAG 3772
QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db 3773 CCCCCCTGGTCCCTCTGCTCCACTAGTCTGTGCAACCTCAGTTCCAGGGGACCAGGTCCA 3832
QY 1201 AlaThrGly 1203
Db 3833 GCCACTGGG 3841

RESULT 3
US-09-207-857-1
; Sequence 1, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Bumcrot, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: ONV-05001
; CURRENT APPLICATION NUMBER: US/09/207,857
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(3905)
US-09-207-857-1

Alignment Scores:
Pred. No.: 0 Length: 4391
Score: 6248.00 Matches: 1200
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 3
Query Match: 99.62% Indels: 0
DB: 3 Gaps: 0

US-09-990-046-2 (1-1203) x US-09-207-857-1 (1-4391)

QY 1 MetThrArgSerProProLeuArgGluLeuLeuProProSerTyrThrProProAlaArgThr 20
Db 297 ATGACTCGATCGCCGCCCTCTAGAGAGCTGCCCGAGTTACACACCCCGACTCGAAC 356
QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db 357 GCAGCAACCCAGATCCTAGCTGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 416
QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db 417 CAGGCGCTGCTCTTCTCTCGGATGCGGATCCAGAGACATTTGTGGCAAAAGTCTCTT 476
QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleGluThr 80
Db 477 CTGGACTTGTGGCTTTGGGCGCTTGGCCATAGTCTCCCGATGCGCCATTATTAGAGACA 536
QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db 537 AACITGGACAGCTCTGGGTAGAGTGGGACCGGGGTGAGCCAGGAGCTGCATTACACC 596
QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120

Db		1677	TTCTGGCTCGGGAATCGGGTGTGATGACGTATTCTCTGCTGGCGCATGCCCTTCACAGAG	1736
Qy		481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr	500
Db		1737	GCTCTGCTGGCACCCTCTCCAGAGCGCATGGCGAGTGTCTGAGCGACGGGACCC	1796
Qy		501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro	520
Db		1797	AGTGTGCTGATCATCATCAACATGGCGCTTCTCTCATGGTGGCTCGTTCCTCC	1856
Qy		521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540
Db		1857	ATCCCTGGCTCGAGGCTTCTCCCTACAGGGCGCATAGTGGTGGCTGGCATTTGTA	1916
Qy		541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560
Db		1917	GCCTGTGATGCTTCTCCAGCCATCTACGCTTGGACTTACGGGGCGGCACCTGCCAG	1976
Qy		561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
Db		1977	CGCTTGTGATGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG	2036
Qy		581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
Db		2037	CCCCAGGAGCTGGGGACGGGACAGTACCAGTGGGCAATTGCCACCTCCTGACAGTT	2096
Qy		601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db		2097	CAAGGCTTTTACCCACTGTGAGCCAGCAGCAGATGTGTCACCATCTGCTCCCTCCCAA	2156
Qy		621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
Db		2157	GCCACCTGGTGGCCCACTTCTGACCCACTGGGCTCTGAGCTCTTACGCCCTGGAGGG	2216
Qy		641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnIleAlaCysLysSer	660
Db		2217	TCCACAGCGGACCTTGTAGCCAGGAGGAGGACAAAGGACAGGAGCTGCAAGTCC	2276
Qy		661	LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
Db		2277	CTGCCCTGTGGCGCTGGAAATCTTGCCCAATTCGCCCGCTATCAGTTTGCCCGTGTGCTG	2336
Qy		681	LeuGlnSerHisAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700
Db		2337	CTCCAGTCACTGCCAAGCCCATCTGCTGGTGTCTTGTGGTGTCTTCTGCGGCTGAGC	2396
Qy		701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly	720
Db		2397	CTTACGGAGCCACCTTGTGTCAAGACGGCTGGCCCTGACGGATGTGGTGCCTCGGGGC	2456
Qy		721	ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740
Db		2457	ACCAAGAGCATGCCCTTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC	2516
Qy		741	LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis	760
Db		2517	CTGTGACCCAGCGGTGGCTTGTACTACGCCCACTCCCAACGGCCCTCTTTGATCTGCAC	2576
Qy		761	GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr	780
Db		2577	CAGCGCTTCACTTCCCTCAAGCGGTGTGCTGCCCCACCGGCCACCCAGCGACCCCGACCC	2636
Qy		781	TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTyr	800
Db		2637	TGGCTGGACATTTACCGCACTGTGCTACAGGGAACTCAGGCTGCCCTTTGACCAAGGACTG	2696
Qy		801	AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla	820
Db		2697	GCTTCTGGGGCATCACCGGCCACTCGTACCGCAATGGCTCTCGAAGATGGGCGCTGGCC	2756
Qy		821	TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr	840
Db		2757	TACAAGCTGCTCATCCAGACTGGAGAGCCCGCAGAGCTCTGGATTTTACGCCAGCTGACC	2816

QY 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
 Db 2817 ACAGGAAGCTGGTGGACAGAGAGGAGTATTCACCCCGAGCTCTTCTACATGGGGCTG 2876

QY 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
 Db 2877 ACCGTGTGGGTGAGCAGTACCCCTGGTCTGGCAGCCTCACAGGCCAATCTTACCCC 2936

QY 881 ProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
 Db 2937 CCACCTCCTGAATGGCTGCAGACAAATACACACCCAGGGGAGAACCTTCGCATCCG 2996

QY 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
 Db 2997 CCAGCTCAGCCCTGGAGTTGGCCAGTTCCCTTCTGCTGGTGGCCCTCCAGAAACT 3056

QY 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
 Db 3057 GCAGACTTTGTGGAGGCATCGAGGGGCCCGGGCAGCATGCCAGAGCCGGCCAGGCT 3116

QY 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
 Db 3117 GGGGTGCACCCCTACCCAGCGCTCCCTTCTCTCTGGGAACAGTATCTGGGCGCTG 3176

QY 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
 Db 3177 CGCGCTGCTCTCTGCTGGCCGTCTGCATCTCTGTGTGCACTTTCTCTGCTGTGCT 3236

QY 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetThr 1000
 Db 3237 CTGCTGCTCTCAACCCCTGGATGGTGGCTCATAGTGTGCTGCTGGCGATGATGACA 3296

QY 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
 Db 3297 GTGGAACTCTTTGGTATCATGGGTCTTCCTGGGCATCAAGCTGAGTGCATCCCGCTGGT 3356

QY 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
 Db 3357 ATCCTTTGGCCCTCTAGGCATTTGGCTTGGTTCACAGTCCAGCTGCTGGGCTTC 3416

QY 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
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QY 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuMetLeuAlaGlySerHis 1080
 Db 3477 CCCGTGACCATGGGGCCATCTCCACATTCCTGGGTCTGCTCATGCTTGTGGTCCCCAC 3536

QY 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
 Db 3537 TTTGACTTCATTGTAAAGTACTCTTTTGGGGCTGCTGACAGTCTCAGCTCTCGGGCCCTC 3596

QY 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
 Db 3597 CTCATGAGACTCGTGTGCTGTGCTGTGCTGTCTCATCTCGGGCCGCCGCCAGAGGTG 3656

QY 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGly 1140
 Db 3657 ATACAGATGTACAAGAAAGCCAGAGATCTCTGAGTCCACAGCTCCACAGGGAGCGGG 3716

QY 1141 LeuArgTyrPglValAspSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
 Db 3717 CTTAGGTGGGGGCATCTCTCTCTGCCCCAGAGCTTTGGCAGAGTGAATACCTCCCATG 3776

QY 1161 ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
 Db 3777 ACCGTGGGCATCAACCCACCCCTGCTGCTGCTGCTATCATCCAGCCCTCATGAG 3836

QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
 Db 3837 CCCCTTGGTCCCTGCTGCACTAGCTGTGGCAACCTCAGTTCCAGGGGACCAAGTCCA 3896

QY 1201 AlaThrGly 1203
 Db 3897 GCCACTGGG 3905

RESULT 4
 US-09-909-280A-1
 ; Sequence 1, Application US/09909280A
 ; Patent No. 6605700
 ; GENERAL INFORMATION:
 ; APPLICANT: Bumcrot, David A.
 ; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
 ; TITLE OF INVENTION: THERETO
 ; FILE REFERENCE: CIBT-P02-050
 ; CURRENT APPLICATION NUMBER: US/09/909,280A
 ; CURRENT FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: US 09/207,857
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR APPLICATION NUMBER: US 60/067,940
 ; PRIOR FILING DATE: 1997-12-08
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 4391
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (297)..(3905)
 US-09-909-280A-1

Alignment Scores:
 Pred. No.: 0 Length: 4391
 Score: 6248.00 Matches: 1200
 Percent Similarity: 99.75% Conservative: 0
 Best Local Similarity: 99.75% Mismatches: 3
 Query Match: 99.62% Indels: 0
 DB: 4 Gaps: 0

US-09-990-046-2 (1-1203) x US-09-909-280A-1 (1-4391)

QY 1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
 Db 297 ATGACTTCGATCGCCGCCCTCAGAGAGCTGCCCGGAGTTACACACCCCGAGTCAAGC 356

QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
 Db 357 GCAGCACCCACAGATCTAGCTGGGAGCTGAGGGCTCCACTCTGGCTTCTGCTTACTTC 416

QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 Db 417 CAGGGCCTGCTCTCTCTGGGATCGGGATCCAGAGACATTGTGGCAAGTGCTCTTT 476

QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
 Db 477 CTGGAGACTGTGTGGCTTTGGGGCCCTGGCATTTAGTCTCCGATCGCCATTATTGAGACA 536

QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
 Db 537 AACTTGGAAACAGCTCTGGGTAGAGTGGGACCGGGGTGAGCCAGAGCTGCTATTACACC 596

QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 Db 597 AAGGAGAAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCCGACGC 656

QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 Db 657 CAGGAGGAGAGACATCTCACACCCGAGACATTGGCCCTCCACCTCCAGGAGCCCTC 716

QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 Db 717 ACTGCCAGTAAGTCCAAGTATCACTCTATGGGAGTCTCTGGGATTTGAACAAATATCGC 776

QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180

Db	777	TACAAAGTCAGAGAGTTCCTCCCTTATGAAATGAATGATTCAGCGAGTGTGAGAGCTG	836	Db	1857	ATCCCTCGCGCTCGAGACCTTCTCCCTACAGCGCGCCATAGTGGTGGCTGCACCTTTGTA	1916
Qy	181	PheProCysValIleLeuThrProLeuAspCysPheTIPGluGluAlaLysLeuGlnGly	200	Qy	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560
Db	837	TTTCCGTGGTGATCTCTACCCCTCCGACTGCTTCTGGAGGAGGCCAAACTCCAAAGG	896	Db	1917	GCGTGATGCTGTCTTCCAGCCATCTTCAGCTTGAGACTTACGGGGGGCCACTGCCAG	1976
Qy	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTIPrThAsnLeuAspProGluGln	220	Qy	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
Db	897	GGCTCCGCTACCTGCGCGCGCGGATATCCAGTGAGCAACCTGGATCCAGAGCAG	956	Db	1977	CGCCTTGATGCTCTCTGCTGCTTCTCCAGTCCCTGCTGCTCAGGTGATTCAGATCCTG	2036
Qy	221	LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGlnLeuLeuAspLys	240	Qy	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
Db	957	CTGCTGGAGAGCTGGGTCCCTTTGCTCTCTGAGGGCTTCGGAGCTGTAGACAAG	1016	Db	2037	CCCCAGGAGCTGGGGACGGGACAGTACCAAGTGGGCAITGCCACCTCTACTGCCAGATT	2096
Qy	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys	260	Qy	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln	620
Db	1017	GCACAGTGGGCGAGGCTAGGTGGGGGCGCCCTGTCTGCACCCTGATGACCTCCACTGC	1076	Db	2097	CAAGCCCTTACCACATGTGAGGCCAGCAGCAGATGTGTCACCATCTGCTCTCCCAA	2156
Qy	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280	Qy	621	AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
Db	1077	CCACCTAGTGCCCCCAACCATCAGCAGCAGGCTCCCAATGTGCTCAGGAGCTGAGT	1136	Db	2157	GCCACCTGCTGGTCCCTCCCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGG	2216
Qy	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTIPrGlnGluGluLeuLeuGly	300	Qy	641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaLysLysSer	660
Db	1137	GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCATGCCAGAGGAAATTGCTGTGGGA	1196	Db	2217	TCCACACGGGACCTTCTAGGCCAGGAGGAGACAAAGCAGAGCAGCCTGCAGATCC	2276
Qy	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320	Qy	661	LeuProCysAlaArgTIPrAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
Db	1197	GGCATGGCCAGAGACCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC	1256	Db	2277	CTGCCCTGTGCCCGCTGGAACTTTCGCCCATCTTCCCGCTATCAGTTTGGCCCTGTGCTG	2336
Qy	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340	Qy	681	LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700
Db	1257	TTCTCTGATGATCCCGCCAGCTGTACAGCATTTCCGGGGTGACTATCAGACACATGAC	1316	Db	2337	CTCCAGTTCACATGCCAAGGCCATCTGCTGGTGTCTCTTGGTGTCTCTTCTGGGCTGAGC	2396
Qy	341	IleGlyTIPrSerGluGluGlnAlaSerThrValLeuGlnAlaTIPrGlnArgPheVal	360	Qy	701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaIleuThrAspValValProAspGly	720
Db	1317	ATTGGCTGGAGTGAGGAGCGGCAGCACAGTGTCTACAAGCTGGCAGCGCGCTTGTG	1376	Db	2397	CTCTACGGAGCCACTTGGTGAAGCGGCTGGCCCTGACGATGTGGTGCTTCGGGGC	2456
Qy	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380	Qy	721	ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740
Db	1377	CAGCTGCCCCAGGAGGCCCTGCCTGAGAACGCTTCCAGCAGATCCATGCTCTCTCTCC	1436	Db	2457	ACCAAGAGCATGCTTCTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGCC	2516
Qy	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400	Qy	741	LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis	760
Db	1437	ACCACCTGTGATGACATCCTGCATGCTTCTGAACTCATGTGCTGCCCGTGGTGGGA	1496	Db	2517	CTGGTGACCCAGGGTGGCTTTGACTAGCCCACTCCCAACGCGCTCTTGTGATCTGCAC	2576
Qy	401	GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTIPrAspCysAlaGln	420	Qy	761	GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr	780
Db	1497	GGCTATCTGCTCATGCTGGCTATGCTGTGACCATGTGCGGTGGGACTGGCGCCAG	1556	Db	2577	CAGCGCTTCAGTTCCTCAAGCGCGTGTCTGCCCCCAACCGGCCACCCAGGACCCCGCACC	2636
Qy	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaSerGly	440	Qy	781	TIPrLeuHisTyrTyrArgAsnTIPrLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTIPr	800
Db	1557	TCCAGGGTTCCGnGGGCTTCCCGGGGTACTGTGTGGGCTTGGCGGTGGCTCAGGC	1616	Db	2637	TGGCTGGCACHATTACCGCAACTGGCTACAGGGAAATCCAGGCTGCTTGTGACAGACTGG	2696
Qy	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro	460	Qy	801	AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla	820
Db	1617	CTTGGGCTGTGTGCTGCTCGGATCACCCTTCAATGTGCTGCTACCCAGGTGCTGCC	1676	Db	2697	GCTTCTGGCGCATCACCCGCCACTCTGTACCGCAATGGCTCTGAAGATGGGCGCTGGCC	2756
Qy	461	PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu	480	Qy	821	TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr	840
Db	1677	TTCTTGGCTCTGGGAATCGGGCTGGATGACGTATTCTCTGCTGGCGCATGCTTCCAGAG	1736	Db	2757	TACAAGCTGCTATCCAGACTGGAGCGCCAGAGGCTCTCGGATTTTCAGCCAGCTGACC	2816
Qy	481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr	500	Qy	841	ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu	860
Db	1737	GCTCTGCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACCGGCACC	1796	Db	2817	ACAAGGAGCTGGTGGACAGAGGGGACTGATTCACCCGAGCTCTTCTACATGGGCTG	2876
Qy	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro	520	Qy	861	ThrValTIPrValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro	880
Db	1797	AGTGTGCTGCTACATTCATCAACAACTATGGCCGCTTCTCATGGTGGCTCTGTTCCC	1856	Db	2877	ACCCTGTGGGTGAGCAGTGCACCCCTGGTCTGGCAGCCTCACAGGCCAACTTCTACCCC	2936
Qy	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540	Qy	881	ProProGluTIPrLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro	900
Db				Db	2937	CCACCTCTGAATGGCTGCAGCAAAATACGACACCCAGGGGGAGAACCTTCGATCCCG	2996

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QY 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2997 CCAGCTCAGCCCTGGAGTTGGCCAGTCCCTTCCTGCTGCTGGCCCTCCAGAGACT 3056
QY 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 3057 GCAGACTTTGTGGAGGCATCATAGGGGGCCCGGGCAGCATGCGCAGAGCGCGCGAGCT 3116
QY 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheThrPheGluGlnTyrLeuGlyLeu 960
Db 3117 GGGGTGCACGCCCTACCCACGGCTCCCTTCCTCTCTGGGAACAGTATCTCTGGGCGCTG 3176
QY 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 3177 CGGCGCTGCTTCCTGCTGGCGCTCATCTGCTGCTGGTGCATCTTCCTCTGCTGCTGCT 3236
QY 981 LeuLeuLeuLeuLeuAsnProThrPheAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db 3237 CTGCTGCTCTCAACCCCTGGATGGCTGGCTCATAGTGTGCTCTCTGGCGATGATGACA 3296
QY 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLeuLeuSerAlaIleProValVal 1020
Db 3297 GTGGAATCTTTGTATCATGGGTTTCTGGGATCAAGGTGATGCTGCTGCTGCTGCTGCT 3356
QY 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
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QY 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3417 CTGACACCCAGGGCAGCCGGAACCTGCGGGCGCCCATGCCCTTGAGCACACATTTGCC 3476
QY 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
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QY 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db 3537 TTTGACTTTCATTGTAAGTACTTCTTTGGGGCTGACAGTCTCACGCTCTGGGGCCCTC 3596
QY 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
Db 3597 CTCATGGACTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3656
QY 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProAlaProGlnGlyGly 1140
Db 3657 ATACAGATGTAACGAAAGCCAGAGATCTCTGAGTCCACCGCTCCACAGGGAGCGGG 3716
QY 1141 LeuArgTyrPheAlaSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db 3717 CTTAGGTGGGGGATCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3776
QY 1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db 3777 ACCGTGGCCATCCACCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3836
QY 1181 ProProTyrProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
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QY 1201 AlaThrGly 1203
Db 3897 GCCACTGGG 3905

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RESULT 5

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US-09-293-505-8
; Sequence 8, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2

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; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 8
; LENGTH: 4004
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-293-505-8

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Alignment Scores:

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Pred. No.: 0 Length: 4004
Score: 3955.00 Matches: 847
Percent Similarity: 65.81% Conservative: 2
Best Local Similarity: 65.66% Mismatches: 10
Query Match: 63.06% Indels: 434
DB: 3 Gaps: 10

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US-09-990-046-2 (1-1203) x US-09-293-505-8 (1-4004)

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QY 101 LysGluLysLeuGlyGluGluAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db 11 CGGAGAGAGCTGGGGAGGAGGCTGCATACCTCTCAGATGCTGATACAGACCGCAGC 70
QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
Db 71 CAGGAGGAGAGAACATCTCTCACCCGGAAGCACCTTGGCTCCACCTCCAGGAGGCCCTC 130
QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 131 ACTGCCAGTAAAGTCCAGTATCACTCTATGGAGTCTCTGGGATTTGAACAAAATCTGC 190
QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db 191 TACAGTCAAGAGTTCCTCTTATGAAATGAAATGATTGAGCGGATGATTGAGAAAGCTG 250
QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyValLysLeuGlnGly 200
Db 251 TTTCCGTGGTGCATCTCTCACCCCTCTGACTCTCTTGGAGGAGGCCAAATCTCCAAGG 310
QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db 311 GGTCTCGCTACTCTGCGCT----- 330
QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 330 ----- 330
QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
Db 330 ----- 330
QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 331 -----CCCAATGTGCTCACGAGCTGAGT 354
QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
Db 355 GGGGGTGGCTGCTTCTCCCAAAATTCATGACATGCGAGGAGAAATTCGCTGGGA 414
QY 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 415 GGCATGGCCAGAGACCCCAAGAGAGCTGCTGAGGGCAGAGGCCCTTCAGAGCACCTTC 474
QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 475 TTGCTGATGAGTCCCGCCAGCTGTACGAGCATTTCCGGGGTGTACTATCAGACATGAC 534
QY 341 IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal 360
Db 535 ATTGGTGGATGAGGAGCGCCAGCACAGTGTCTAAGCCTGGCAGCGCGCTTTGTG 594

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Db 595 CAGGTGGTATGACAAAGACAGGGGGTGCCTCAGGCCATTCCCTCCTCCTGCCCCCT 654
QY 361 -----GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnG 374
Db 655 CCAATCCACCCCTGTTCTCCAGCTGGCCAGAGGCCCTGCTGAGAACGCTTCCAGCA 714
QY 374 nileHisAlaPheSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
Db 715 GATCATGCTTCTCTCCACACCCCTGATGACATCCTGCATGCGTCTCTGAAGTCAG 774
QY 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet----- 405
Db 775 TGCTGCCCGTGTGGTGGAGGCTATCTGCTCATGTGGTGTCTTGCACTGGCACCTTGCC 834
QY 405 ----- 405
Db 835 CCCACCCACCTCCAAACAGTGCCCAACCCCTGGGGAGCCCTGAGACTGCCCTTTCCTCCC 894
QY 406 ----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
Db 895 ACAGCTGGCTATGCTGTGTGACCATGCTGCGGTGGACTGCGCCCAAGTCCCCAGGGTTC 954
QY 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCTTGGCGGGTACTGCTGTGGCCCTGGCGGTGGCTCAGGCTTGGGCTCTG 1014
QY 444 sAlaLeuLeuGlyIleThrPheAsnAlaIaThr----- 456
Db 1015 TGCCCTGCTCGGCATCACCTTCAATGCTGCCACTCCAGGTAGCCGAGGACTGCAGGGC 1074
QY 457 -----G 457
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Db 1135 AGGTGTGCTTCTTGAAGTCTGGGAATCGCGTGGATGATGATGATGATGATGATGATG 1194
QY 477 laPheThrGluAlaLeuProGlyThr----- 485
Db 1195 CCTTCACAGAGGCTCTGCTCGGCAACCCCTCTCCAGGTGGGGCTGTTCCTCCAGGGGTCA 1254
QY 485 ----- 485
Db 1255 TCTGAGGCAGCTCAGCTTACTGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA 1314
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QY 485 ----- 485
Db 1495 CAAGTTCCTGAGCCTCCCTTCACTCCACTTTGACAGGGCCCTCCTTGTGACTGAGG 1554
QY 486 -----ProLeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyT 500
Db 1555 GCAGGTCCCACTCTGTCTCTGG-CAGGAGCGCATGGGCGAGTGTCTGACGGCAGGGCA 1613
QY 500 hrSerValValLeuThrSerIleAsnAenMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CCAGTGTGTACTCACATCCATCAACAACATGGCGGCTTCTCTCATGTGCTGCCCTCGTTC 1673
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QY 520 roileProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTCGCTGCGAGCCITCTCC----- 1699
QY 540 alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgHisCys 559
Db 1700 -----CTACAGCTTGACCTACGGCGGCCACTGCG 1730
QY 560 GlnArgLeuAspValLeuCysCysPheSer----- 569
Db 1731 CAGCGCTTGATGTGCTGCTGCTTCTC-CAGGTACTCCCTGGCGGCCCGAGCCCTTCCT 1789
QY 569 ----- 569
Db 1790 CCGGTGACCCAGCCAGCCTGTCCCTCACCAGCATTTTCAAGGCACAGACCTGTGTCATCCA 1849
QY 570 -----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTCTTCCAGTCCCTGCTGCTCAGGTGATTCAGATCCTGCCCCAGGAGCTG 1909
QY 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGGACGGACAGTACAGTGGGCAATGCCACCTCCTGCTGCCACAGTTCAGGCTTTACC 1969
QY 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAGCCAGCAGCCAGCATGTGGTCCACATCTGCTCCCAAGCCACCTGGTG 2029
QY 625 ProProSerSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCACTGGGCTCTGAGCTCTTCAGGCTTGGAGGCTCCACAGGGAC 2089
QY 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTTCTAGGCGAGGAGGAGAGCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2149
QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
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QY 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuGlyAla 704
Db 2210 GCCAAGGCCATCTGCTGTGTGCTCTTTGTTGCTCTTCTGGGCTGAGCCTCTACGGAGCC 2269
QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGGTGCAAGAGCGCCTGGCCCTGACGGATGTGTGCTCGGGCACCAGAGGACAT 2329
QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCCTTCTGAGCGCCAGCTCAGTACTTCTCCTGTACGAGGTGGCCCTGGTGACCCAG 2389
QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
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QY 765 SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
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QY 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2510 TACCGCACTGGCTACAGGGAATCCAGGCTGCCCTTTGACCAGGACTGGGCTTCTGGGCGC 2569
QY 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2570 ATCACCAGCCACCTGATCCGCAATGGCTCTGAGGATGGGCGCTTGGGCTTACAGCTGCTC 2629
QY 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer----- 837
Db 2630 ATCCAGACTGGAGACGCCAGGAGGCTCTGGATTTTCCAGCCAGGTTGGGAGGGCTGGAG 2689
QY 837 ----- 837
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QY      838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuLeuProGluLeuPhe 856
Db      2750 CTGAGCTGACCAAGAAGACTGGTGACAGAGAGGAGCTGATTCACCCGAGCTCTTC 2809
QY      857 TyrMetGlyLeuThrValTTPValSerSerAspProLeuGlyLeuAlaSerGlnAla 876
Db      2810 TACATGGGCTGACCGTGGTGAGCAGTACCCCTGGGTCTGGCAGCCTCACAGGCC 2869
QY      877 AsnPheTyrProProProGluThrLeuHisAspLysTyrAspThrThrGlyGluAsn 896
Db      2870 AACTTCTACCCCCACCTCTGAATGCTGCAGCAAAATACGACACACCGGGGGAAC 2929
QY      897 LeuArg----- 898
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QY      898 ----- 898
Db      2990 GAGCCTGAGCCCTGCCACTCTGCCCGTGCTACCGCCCTGTCCCTCTCCCTTTCTC 3049
QY      899 -----lleProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db      3050 CTTCCCTCCCTCCACAGTCCCGCAGCTCAGCCCTTGAGTTTGCCTCAGTTCCCTT 3109
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Db      3110 CTGTCTGGTGGCTCCAGAAAGACTGCAGACTTTGTGGAGGCCATCGAGGGGGCCCGGC 3169
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Db      3170 AGATGGCAGAGCGCGCAGCTGGGGTGCAGCGCTACCCAGCGGCTCCCTCTCCT 3229
QY      952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
Db      3230 CTTCTGGGAACATATCTGGGCTGGCGGCTGCTTCTCTGCTGGCGCTGTGCATCTGCT 3289
QY      972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 992
Db      3290 GGTGTGCACTTCTCTGCTGTCTCTGCTGCTCTCTCAACCCCTGGAACGCTGCGCTCAT 3349
QY      992 e----- 992
Db      3350 AGTGAGTGCTTGAGAGTGGGACAGACACCCACCCCTTCCCTGCGCCAGCTGTCTAT 3409
QY      993 -----ValLeuValLeuAlaMetM 999
Db      3410 CCTCTCTGCCAGGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGTGCTGGCGATGA 3469
QY      999 eThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
Db      3470 TGACAGTGAACCTCTTGTGTATCATGGGTTCCTGGGCAATCAAGCTGAGTGCCATCCCG 3529
QY      1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
Db      3530 TGGTGATCCTTGGGCTCTGTAGGCAATTGGCGTTGAGTTTCAAGTCCACGCTGGCTCTGG 3589
QY      1039 lYPheLeuThrThrGlnGly 1045
Db      3590 TGAGCACGGGACCCCGGGG 3609

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RESULT 6

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US-09-060-939A-8
; Sequence 8, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

```

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; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4004 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; US-09-060-939A-8

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Alignment Scores:
Pred. No.: 0 Length: 4004
Score: 3955.00 Matches: 847
Percent Similarity: 65.81% Conservative: 2
Best Local Similarity: 65.66% Mismatches: 10
Query Match: 63.06% Indels: 434
DB: 4 Gaps: 10

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US-09-990-046-2 (1-1203) x US-09-060-939A-8 (1-4004)

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QY      101 LysGluLysLeuGlyGluGluAlaTyrThrSerGlnMetLeuLeuGlnThrAlaArg 120
Db      11 CGGGAGAGCTGGGGAGGAGGCTGCATACCTCTCAGATGCTGATACAGACCGACGC 70
QY      121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
Db      71 CAGGAGGAGAGAACATCTCTCACCCGAGCACCTTGGCTCCACCTCCAGGAGGCCCTC 130
QY      141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db      131 ACTGCCAGTAAAGTCCAGTATCACTCTATGGAGTCTCTGGGATTTGAACAAATCTGC 190
QY      161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db      191 TACAAGTCAGGAGTTCCTCTTATTGAAATGGAATGGAATGAGCGGATGATTGAGAAGCTG 250
QY      181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db      251 TTTCCGTGCGTATCTCTCACCCCTCTCGACTCTTCTGGGAGGGAGCCAACTCCAGGG 310
QY      201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db      311 GGCTCCGCTACCTGCCGCT----- 330
QY      221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db      330 ----- 330
QY      241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
Db      330 ----- 330
QY      261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280

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Db 331 -----CCCAATGTGGCTCAGGAGTGAGT 354
QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTyrGlnGluGluLeuLeuGly 300
Db 355 GGGGGTGCATGGCTTCTCCACAAATTCATGCACTGGCAGGAGAAATGTGCTGGGA 414
QY 301 GlyMetAlaArgAspProGlnGlyLeuLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 415 GGCATGGCCAGAGACCCCAAGAGAGCTGCTGAGGGCAGAGGCCCTGCAGACACCTTC 474
QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 475 TTGCTGATGAGTCCCGCCAGCTGTACGAGCAITTCGGGGTGACTATCAGACACATGAC 534
QY 341 IleGlyTyrSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 535 ATTGGCTGGAGTGAGGAGCAGGCCAGACAGTGTCTAAGCCTGGCAGCGCGCTTTGTG 594
QY 360 ----- 360
Db 595 CAGGTCGGTATGACAAGAGACAGGGGGTGCCCTGAGGCCATTCCTCTCTGCCCCCT 654
QY 361 -----GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnI 374
Db 655 CCTATCCACCTGTTCTCAGCTGGCCAGAGGCCCTGCTGAGAACGCTTCCCGCA 714
QY 374 nileHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValse 394
Db 715 GATCCATGCTTCTCTCCACCACTGGATGATCATCTGCATGCGTCTCTGAAAGTCAG 774
QY 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet----- 405
Db 775 TGTGCCCGTGTGGTGGAGGCTATCTGCTCATGTGGTGGTCTTGCACTGGCACCTGGCC 834
QY 405 ----- 405
Db 835 CCACACCCACTCCAAACCACTGCCACCCCTGGGGAGCCCTGAGACTGCCCTTCCCCCC 894
QY 406 ----LeuAlaTyrAlaCysValThrMetLeuArgTyrAspCysAlaGlnSerGlnGlyse 424
Db 895 ACAGCTGGCCATATGCTGTGTGACCAATGCTGCGTGGGACTGGGCCCACTCCAGGGTTC 954
QY 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCTTGGCCGGGTACTGCTGTGTGGCCCTGGCGGTGGCCCTCAGGCTTGGGCTCTG 1014
QY 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThr----- 456
Db 1015 TGCCCTGCTCGGCATCACCTTCAATGTGCGCACTTACCAGGTACGCCAGGACTGCAGGGC 1074
QY 457 -----G 457
Db 1075 AGACTCAGTGCCAGTCACACCGCTTCACGGGTCTCAGCTGCCCGCTCTCTGCCCTCC 1134
QY 457 lnValLeuProPheLeuAlaGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
Db 1135 AGGTGCTGCCCTCTTCGACTCTGGAAATCGCGTGGATGACGTAITCTGCTGGCGCATG 1194
QY 477 laPheThrGluAlaLeuProGlyThr----- 485
Db 1195 CCTTCACAGAGGCTCTGCTGGCACCCCTCTCCAGGTGGGSCCTTGTCCCCCAGGGTCA 1254
QY 485 ----- 485
Db 1255 TCTGAGGCAGCTCAGCTTACTGTGTTAAGAGCTCTTGTTCAAGTGACCTTGGGCTGCTA 1314
QY 485 ----- 485
Db 1315 ATGAACCTCGGTGCTCTGTGCCCCATGTGTAAACAGGGGAAATAATAGTCTGTGCTCT 1374
QY 485 ----- 485
Db 1375 AAGGTTATTCTTTGGATCAGTGAAGTAACCTCAAGTTGAATGCTTAGAACAAGCCCATCAT 1434

QY 485 ----- 485
Db 1435 ACGTACATGGTACCCCAATAAATGTAGCCACCTGTGTATGACTGCCCCACCTCTGCACCC 1494
QY 485 ----- 485
Db 1495 CAAGTTCTGAGCCTCCCTTCCACTCCACTTTTGACACGGCCCTCCCTTGTGACCTGAGG 1554
QY 486 -----ProLeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyT 500
Db 1555 GCAGGTCCCACCTCTGCTCTGG--CAGGAGCGATGGCGAGTGTCTGCAGCGCACGGGCA 1613
QY 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CAGTGTGTGTACTCATCATCAACATGCGCCCTTCTCTCATGGCTGCCCTCGTTC 1673
QY 520 roileProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCTTCTCC----- 1699
QY 540 alAlaValMetLeuValPheProAlaIleLeu--SerLeuAspLeuArgArgHisCys 559
Db 1700 -----CTACAGCCTGGACCTACGGCGGCCACTGC 1730
QY 560 GlnArgLeuAspValLeuCysCysPheSer----- 569
Db 1731 CAGCGCTTGTGTGTCTGCTGCTTCTC--CAGGTACTGCTGGGCCAGCCCTTCCT 1789
QY 569 ----- 569
Db 1790 CCGGTGACCCAGCCAGCCTGCTCCCTCACCAGCATTTCAAGGCACACAGACTGTGATCCA 1849
QY 570 -----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTTCTCCAGTCCCTGCTCTGCTCAGTGATTCAGATTCCTGCCCGGAGCTG 1909
QY 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGAGCGGACAGTACAGTGGCANTGGCCACTCCTCAGTCCACAGTTCAGGCTTTACC 1969
QY 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCAGCATGTGGTCACCATCTGCTCCCAAGCCACCTGGT 2029
QY 625 ProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTACGCCCTGGAGGCTCCACACGGAC 2089
QY 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTCTAGCCAGAGGAGGAGACAGGCAGAGGCTGCAAGTCCCTGCCCTGTGCC 2149
QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
Db 2150 CGCTGGAATCTTGCCCAATTCGCCGCTATCAGTTTCCCCGTTGTGCTCCAGTCACT 2209
QY 685 AlalysAlaIleValLeuValLeuPheGlyValAlaLeuGlyLeuSerLeuTyrGlyVala 704
Db 2210 GCCAAGGCCATCGGTGGTGTCTTTGGTGTCTTCTGGGCCCTGAGCCCTCTACGGAGCC 2269
QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGTGCAAGACGCGCTTGGCCCTGACGATGTGTGTGCTCGGGGCACCAAGGAGCAT 2329
QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCCTTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTTGTGACCCAG 2389
QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2390 GGTGGCTTTGACTAGGCCCTCTCCAAAGCGGCCCTCTTTGATCTGACACAGCGCTTCAGT 2449

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Qy 765 SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2450 TCCCTCAAGGGGGTGTGCCCCACCCGCGCCACCCAGGACCCCGCAGCTGCTGCACTAT 2509
Qy 785 TyrArgLenTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2510 TACGCGCAACTGGCTACAGGGAATCCAGGCTGCCCTTGACAGGACTGGGCTTCTGGGCGC 2569
Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2570 ATCACCAGCCCACTCGTACCGCAATGGCTCTGAGATGGGGCCCTGGCCTACAAGCTGCTC 2629
Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer----- 837
Db 2630 ATCCAGACTGGAGAGCGCCAGGAGCCCTCGATTTTCAGCCAGGTGGGAGAGGCTGGAG 2689
Qy 837 ----- 837
Db 2690 GGGTCCACTAGTACAGGGGCTGCAGGCTCTCTGGGCGCCAGGCTTCAGCCCTCTGCTC 2749
Qy 838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
Db 2750 CTGAGCTGACCAAGAGAGCTGGTGACAGAGGAGCTGATTCACCCGAGCTCTTC 2809
Qy 857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
Db 2810 TACATGGGGCTGACCGGTGGGTGAGCAGTGACCCCTGGGTCTGGCAGCCTTCACAGGCC 2869
Qy 877 AsnPheTyrProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
Db 2870 AACTTCTTACCCCGCACCTCTGAATGGCTGCACGACAAATACGACACACCGGGGAGAAC 2929
Qy 897 LeuArg----- 898
Db 2930 CTTGCGCAGTGAGCTTGGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCAACAAGCCCT 2989
Qy 898 ----- 898
Db 2990 GAGCCTGAGGCCCTGCCCACTCTGCCCGGTGCTCACGGCCCTGTCCCTCTCCCTCTCTC 3049
Qy 899 -----IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db 3050 CCTTCCCTCCCTCCACAGTCCCGCCAGCTCAGCCCTTGGAGTTGGCCAGTTCCCTT 3109
Qy 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db 3110 CTTGCTGCGGGCTCCAGAGAGCTCGAGACTTGTGGAGGCCATCGAGGGGCGCCGGGC 3169
Qy 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db 3170 AGCATGCGCAGAGCGCGCCAGGCTGGGTGCGAGCTACCCAGCGGCTCCCTCTTCTCT 3229
Qy 952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
Db 3230 CTTCTGGGAACAGTATCTGGGCTCGCGGCTGCTCTCTGCTGGCGTCTGCACTCTGCT 3289
Qy 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuL 992
Db 3290 GGTGTGCATTTCTCTGTCTGTCTGTGTCTCTCAACCCCTGAGCGCTGGCCCTCAT 3349
Qy 992 e----- 992
Db 3350 AGTGAGTGCTTGAGGAGTGGGACAGAGACACCCACCCCTTCCCTGCGCCAGCTCTCAT 3409
Qy 993 -----ValLeuValLeuAlaMetM 999
Db 3410 CCTCTCTGCCAGGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGGTCTCGCGCATGA 3469
Qy 999 eTrpValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProv 1019
Db 3470 TGACAGTGAACCTTTTGTGTATCATGGTTTCTGGGSCATCAAGCTGAGTGCCATCCCG 3529
Qy 1019 aIValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039

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Db 3530 TGGTGATCCCTGTGGCCCTCTGTAGGCATTTGGCTGTAGTTCCACAGTCCACGCTGCTGG 3589
Qy 1039 lyPheLeuThrThrGlnGly 1045
Db 3590 TGACACGGGCACCCCGGGG 3609

RESULT 7
US-09-293-505-9
; Sequence 9, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: PI405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 9
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-293-505-9

Alignment Scores:
Pred. No.: 1,546-308 Length: 2082
Score: 3387.00 Matches: 656
Percent Similarity: 96.33% Conservative: 1
Best Local Similarity: 96.19% Mismatches: 3
Query Match: 54.00% Indels: 23
DB: 3 Gaps: 2

US-09-990-046-2 (1-1203) x US-09-293-505-9 (1-2082)

Qy 1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
Db 8 ATGACTCGATCGCGCCCTTCAGAGAGCTGCCCGGAGTTACACACCCCGAGCTCGAACC 67
Qy 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db 68 GCAGCACCCCGAGATCTCTAGCTGGGAGCCCTGAAGGCTCCACTCTGGCTTCGTGCTTCT 127
Qy 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db 128 CAGGGCTGCTCTCTCTCTCTGGGATGCGGATCCAGAGACATTTGTGGAAAGTGCTCTTT 187
Qy 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
Db 188 CTGGGACTGTGGCCCTTGGGCGCTTGGCATTTAGGTCTCCGCATGGCCATTATTGAGACA 247
Qy 81 AsnLeuGlnGlnLeuTrpValGluValGlySerArgValSerGlnLeuHisTyrThr 100
Db 248 AACTTGGAAACAGCTCTGGGTAGAGTGGCAGCCGCGGTGAGCAGGAGTGCATTACACC 307
Qy 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetIleIleGlnThrAlaArg 120
Db 308 AAGGAGAGCTGGGGAGGAGGCTGCATACACTCTCAGATGCTGATACAGACCGCACGC 367
Qy 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
Db 368 CAGGAGGAGAGAACATCTCACACCCGAGCATTGGCTCCACTCCAGCAGCCCTC 427
Qy 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 428 ACTGCCAGTAAAGTCCAAAGTATCACTCTATGGAAGTCTCTGGGATTTGAACAAATCTGC 487
Qy 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db 498 TACAAGTCAGGAGTTCCCTTTATTGAAATGGAATGATTTGAGTGGATGATTGAGAAGCTG 547

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QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpClnGlyAlaLysLeuGlnGly	200	Db	1600	-----ATCCTCAGCCTGGACCTACGGGGGGCCCACTGCCAG	1635
Db	548	TTTCCTGGGTGATCTCAACCCCTCGACTGCTTCTGGAGGGAGCCAACTCCAAAGGG	607	QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
QY	201	GlySerAlaIleLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220	Db	1636	CGCCTTGTATGTCTGCTGCTTCTCCAGTCCCTGCTGCTGCTCAGTGATTTCAGATCCTG	1695
Db	608	GGCTCGCCTACTCTGCCCGCCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG	667	QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
QY	221	LeuLeuGluGlnLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240	Db	1696	CCCCAGAGCTGGGACGGGACGACGATACAGTGGGATTCGCCACCTCCTGCGCCAGATT	1755
Db	668	CTCTGGAGAGCTGGGTCTCTTTCCTCCCTTGGAGGGCTTCGGGAGCTGTAGACAAG	727	QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln	620
QY	241	AlaGlnValGlyGlnAlaIleValGlyArgProCysLeuHisProAspAspLeuHisCys	260	Db	1756	CHAGCCTTTACCCACTGTGAAGCCAGCAGCAGCATGTGTGTCACCATCTCTGCTCCCAA	1815
Db	728	GCAAGGTGGCCAGGCTACGTGGGGCGCCCTGCTCTGACCTGTATGACCTCCACTGC	787	QY	621	AlaHisLeuValProProProSerAspProLeuGlySerClnLeuPheSerProGlyGly	640
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280	Db	1816	GCCACCTGTGTGCCCCACCTTCTGACCCCACTGGGTCTGAGCTCTTCAGCCCTGGAGGG	1875
Db	788	CCACCTAGTGCCTCCCAACCATCAGCAGGAGGCTCCCAATGTGGCTCAGAGCTGAGT	847	QY	641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer	660
QY	281	GlyCysHisGlyPheSerHisLysPheMethIleTrpGlnGluGluLeuLeuGly	300	Db	1876	TCCACACGGGACCTTTAGCCAGGAGGAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGG	1935
Db	848	GGGGCTGCTCCTCTCCCAAAATTCATGCACTGCGCAGGAGGAAATTCCTGCTGGGA	907	QY	661	LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTrpGlnPheAlaProLeuLeu	680
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuArgAlaGluAlaLeuGlnSerThrPhe	320	Db	1936	CTGCCCTGTGCCCTGGAAATCTTGCCCAT-----TTCGCCCGGGAATTC	1980
Db	908	GGCATGGCCAGAGACCCCAAGGAGAGCTGCTGAGGGCAGAGGCTTCGACAGCACCTTC	967	QY	681	LeuGln 682	
QY	321	LeuLeuMetSerProArgGlnLeuTrpGluHisPheArgGlyAspTrpGlnThrHisAsp	340	Db	1981	CTGCAG 1986	
Db	968	TTGCTGATGAGTCCCGCCAGCTGTACGAGCAATTTCCGGGTGACTATCAGACACATGAC	1027	RESULT 8			
QY	341	IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal	360	US-09-060-939A-9			
Db	1028	ATTGGCTGGAGTAGGAGCAGGCCACACAGTGTCTACAAGCCTGGCAGCGCGCTTTGTG	1087	; Sequence 9, Application US/09060939A			
QY	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380	; Patent No. 6709838			
Db	1088	CAGCTGGCCAGGAGGCGCTGCTGGAGAACCTTCCAGCAGATCCATGCTTCTCTCTCC	1147	; GENERAL INFORMATION:			
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400	; APPLICANT: Frederic de Sauvage, David A. Carpenter			
Db	1148	ACCACCTGGATACATCTGCTGATGCTGCTGAGTCACTGCTGCCCGTGTGGGA 1207	1207	; TITLE OF INVENTION: Patched-2			
QY	401	GlyTrpLeuLeuMetLeuAlaTyAlaCysValThrMetLeuArgTrpAspCysAlaGln	420	; NUMBER OF SEQUENCES: 32			
Db	1208	GGCTATCTGCTCATGCTGGCCTATGCTGTGACCATGCTGCGGTGGGACTGCGGCCAG	1267	; CORRESPONDENCE ADDRESS:			
QY	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly	440	; ADDRESSEE: Genentech, Inc.			
Db	1268	TCCAGGGTTCCGTGGGCTTTCGGGGGTACTGCTGGTGGCCCTGGCGGTGGCTCAGGC	1327	; STREET: 1 DNA Way			
QY	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro	460	; CITY: South San Francisco			
Db	1328	CTTGGGCTCTGCGCTCTCGGCATCACTTCAATGCTGCCACTACCCAGGTCTGCC	1387	; STATE: California			
QY	461	PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu	480	; COUNTRY: USA			
Db	1388	TTCTTGGCTCTGGGAATCGGCTGGATGACGTATTCTCTGCTGGCGCATGCCCTTCACAG	1447	; ZIP: 94080			
QY	481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr	500	; COMPUTER READABLE FORM:			
Db	1448	GCTCTGCTGGACCCCTCTCCAGGAGCGCATGGCGAGTGTCTGACGCGCAGCGGCACC	1507	; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk			
QY	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaLeuValPro	520	; COMPUTER: IBM PC compatible			
Db	1508	AGTGTGCTGACTCACATCATCAACACATGGCGGCTTCTCATGCTGCTGCTGCTGCT	1567	; OPERATING SYSTEM: PC-DOS/MS-DOS			
QY	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540	; SOFTWARE: WinPatin (Genentech)			
Db	1568	ATCCCTGGCTGGCAGCCTTCTCTTACAGCC-----	1599	; CURRENT APPLICATION DATA:			
QY	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560	; APPLICATION NUMBER: US/09/060,939A			
				; FILING DATE: 15-Apr-1998			
				; CLASSIFICATION: 435			
				; ATTORNEY/AGENT INFORMATION:			
				; NAME: Svoboda, Craig G.			
				; REGISTRATION NUMBER: 39,044			
				; REFERENCE/DOCKET NUMBER: P1405			
				; TELECOMMUNICATION INFORMATION:			
				; TELEPHONE: 650/225-1489			
				; TELEFAX: 650/952-9881			
				; INFORMATION FOR SEQ ID NO: 9:			
				; SEQUENCE CHARACTERISTICS:			
				; LENGTH: 2082 base pairs			
				; TYPE: Nucleic Acid			
				; STRANDEDNESS: Double			
				; TOPOLOGY: Linear			
				US-09-060-939A-9			
				Alignment Scores:		1.54e-308	2082
				Pred. No.:		3387.00	656
				Score:			

Percent Similarity: 96.33%
 Best Local Similarity: 96.19%
 Query Match: 54.00%
 DB: 4

US-09-990-046-2 (1-1203) x US-09-060-939A-9 (1-2082)	
QY	1 MetThrArgSerProLeuArgGluLeuProProSerTyrThrProProAlaAatqThr 20
DB	8 ATGACTGATCGCGCCCTCAGAGAGCTGCCCGGAGTTACACACCCAGCTCGAAC 67
QY	21 AlaAlaProGlnLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
DB	68 GCAGCACCCAGATCTTAGCTGGAGCTGAAGGCTCACTCTGCTCTGCTTACTTC 127
QY	41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
DB	128 CAGGGCTGCTCTCTCTGGGATGGGGATCCAGAGACATTTGGCAAAAGTCTCTT 187
QY	61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleLeuThr 80
DB	188 CTGGGACTGTGGCTTTGGGCTTGGGCTTGGCAATAGTCTCCGATGGCCATTTAGACA 247
QY	81 AsnLeuGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
DB	248 AACTTGGAAACAGCTCTGGGTAGAAAGTGGGAGCGGGTGGAGGAGCTGCATTACAC 307
QY	101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
DB	308 AAGGAGAAGCTGGGGAGGAGGTGCATACACCTCTCAGATGCTGTATACAGACGCGACGC 367
QY	121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
DB	368 CAGAGGGAGAGAACTCTACACCCGAAGCACTTGGCCCTCCACCTCCAGGAGCGCCCTC 427
QY	141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
DB	428 ACTGCAGGTAAAGTCCAAAGTATCACTCTATGGGAAGTCTCTGGGATTTGAACAAATCTGC 487
QY	161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
DB	488 TACAAGTCAAGAGTTCCTCTTATGAAATGGAAATGATGAGTGGATGATTGAGAAGCTG 547
QY	181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
DB	548 TTTCCGTGGTATCTCTACCCCTCTGACTGCTCTTGGAGGAGGACCAACTCCAAAGG 607
QY	201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
DB	608 GGCTCCGCTACTGCTCCGCGCGCCCGGATATCCAGTGGACCAACTGGATCCAGAGCAG 667
QY	221 LeuLeuGluLeuLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
DB	668 CTGCTGGAGAGCTGGGTCTCTTGGCTCTCTTGGAGGCTTCCGGAGGCTGTAGACAAG 727
QY	241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
DB	728 GCACAGTGGCCAGGCCCTACGTGGGGCGGCCCTGTCTGACCCCTGATGACCTCCACTGC 787
QY	261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
DB	788 CCACCTAGTGGCCCCCAACCATCACACAGCAGGCTCCCAATGTGGCTCAGGAGCTGAGT 847
QY	281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuLeuGly 300
DB	848 GGGGGCTGCCATGGCTCTCTCCACAAATTCATGCACTGGCAGGAGGAATGCTGCTGGGA 907
QY	301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
DB	908 GGCATGGCCAGAGACCCCAAGAGAGAGCTGTGAGGGCAGAGCCCTGCAGAGACCTTC 967
QY	321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
DB	968 TTGCTGATGAGTCCCCCAGCTGTACAGAGATTTCCGGGGTGACTTACAGACACATGAC 1027
QY	341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
DB	1028 ATTGGCTGGAGTGAGGAGCAGGCACAGTGTCAAGCCCTGSCAGCGCGCTTTGTG 1087
QY	361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
DB	1088 CAGTGGCCCGAGAGGCCCTTGCCTGAGAACGCTTCCAGCAGATCCATGCTTCTCTCC 1147
QY	381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
DB	1148 ACCACCTGTATACATCTCTGATGGTCTCTGAAAGTCACTGCTGCTGCTGGTGGGA 1207
QY	401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
DB	1208 GGCTATCTGCTCATGCTGGCTATGCTGTGTGACCATGCTGCGTGGAGCTGCGCCAG 1267
QY	421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
DB	1268 TCCAGGGTTTCCGTGGGCTTGGCGGGGTACTGCTGCTGGCCCTGGCGGTGGCTCAGGC 1327
QY	441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
DB	1328 CTTGGGCTCTGTGCTGCTGCTGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCC 1387
QY	461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
DB	1388 TTCTTGCTCTGGGAATCGGCGTGGATGAGTATTCTCTGCTGGCGCATGCTTCACAGAG 1447
QY	481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
DB	1448 GCTCTCCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGAGCGGCACGGCACC 1507
QY	501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
DB	1508 AGTGTGCTACTCACATCCATCAACAATGGCGCCCTTCTCTAAGTGTGCTTCTGTTCCC 1567
QY	521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
DB	1568 ATCCCTGGCTGGAGCCCTTCTCTTACAGCC----- 1599
QY	541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
DB	1600 -----ATCCCTCAGCCTGGACCTAGCGCGGCGGCACCTGCCAG 1635
QY	561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
DB	1636 CGCCTTGATGTGCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTGATCCCTG 1595
QY	581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
DB	1696 CCCCAGGAGCTGGGGACGCGACAGTACCAGTGGGCTTCCACCTACTGCCACAGTT 1755
QY	601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
DB	1756 CAAGCCTTTACCCACTGTGAAGCCAGCAGCCAGCATGTGGTCAACCTCTGCTGCCCAA 1815
QY	621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
DB	1816 GCCCACCTGGTGGCCCCCCTTCTGACCCACTGGGCTCTGAGCTCTTTCAGCCCTTGAGGG 1875
QY	641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
DB	1876 TCCACACGGGACCTTCTAGGCCAGGAGGAGGAGACAAGGAGAGGAGCCCTGCAAGTCC 1935
QY	661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
DB	1936 CTGGCCTGTGGCCGCTGGAAATCTTCCCAT-----TTGCCGCCGGAATTC 1980
QY	681 LeuGln 682
DB	1981 CTGCAG 1986

RESULT 9

US-08-540-406-18
Sequence 18, Application US/08540406
Patent No. 5837538
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,406
FILING DATE: 06-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 5288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-540-406-18

Alignment Scores:
Pred. No.: 2,75e-304 Length: 5288
Score: 3349.00 Matches: 662
Percent Similarity: 70.02% Conservative: 200
Best Local Similarity: 53.78% Mismatches: 298
Query Match: 53.40% Indels: 71
DB: 2 Gaps: 16

US-09-990-046-2 (1-1203) x US-08-540-406-18 (1-5288)

QY	12	ProSerTyrThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu---	30
DB	540	CCCAGCTACTGC---GACGCGCGCTTCGCTCTGGAGCAGATTTCCAAAGGGGAAGGCTACT	596
QY	31	-----LysAlaProLeuThrProLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly	48
DB	597	GGCCGGAAGCGCCACTGTGGCTGAGAGCGAAAGTTTCAGAGACTCTTTATTAAACTGGGT	656
QY	49	CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuAlaPheGlyAla	68
DB	657	TGTTACATTCAAAAACCTGCGCAAGTTCTTGTTGGGCCCTCTCATATTGGGGCC	716
QY	69	LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu	88
DB	717	TTCCGCGTGGATTAAAAAGCAGCAACCTCGAGACCAACGTGGAGGAGCTGTGGGTGGAA	776
QY	89	ValGlySerArgValSerGlnGluLeuHisTyrThrLysGlnLysLeuGlyGluAla	108
DB	777	GTTGGAGGACGAGTAAGTCGTGAATTAATATATATCTCGCCAGAGATTTGGAGAGAGCT	836

QY	109	AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr	128
DB	837	ATGTTTAATCCTCACTCATGATACAGACCCCTAAAGAAGAAGGTCTAATGTCCTGACC	896
QY	129	ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer	148
DB	897	ACAGAAGCGCTCTCAACACCTGGACTCGGCACTCCAGGCCAGCCGCTGCCATGTATAC	956
QY	149	LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle	168
DB	957	ATGTACACAGCAGCAGTGGAAATTTGTTTCAAAATCAGAGAGAGTATACACA	1016
QY	169	GluAsnGlyMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuThrPro	188
DB	1017	GAACAGGTTACATGATAGATAATAGATATCTTTACCTTGTTGATTTATACACCT	1076
QY	189	LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg	208
DB	1077	TTGGACTGCTTCTGGGAAGGGCGAAATACAGTCTGGGACAGACATACCTCTAGGTAA	1136
QY	209	ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGlyProPhe	228
DB	1137	CCTCCTTTGGGGTGGACAACTTCGACCCCTTTGGAATCTCTGGAAGAGTTAAGAAATA	1196
QY	229	--AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr	247
DB	1197	AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGGTGGTCATGGTTAC	1256
QY	248	ValGlyArgProCysLeuHisProAspAspLeuHisCysProSerAlaProAsnHis	267
DB	1257	ATGGACCGCCCTGCTCAATCGCGCGATCCAGACTGCCCGCCACAGCCGCCCAACAAA	1316
QY	268	HisSerArgGlnAlaProAsnValAlaHisGluSerGlyGlyCysHisGlyPheSer	287
DB	1317	AATCAACCAACCTCTGATATGGCCCTTTGTAATGGTGATGTCATGCTTATCC	1376
QY	288	HisLysPheMetHisTrpGlnGluGluLeuLeuGlyGlyMetAlaArgAspProGln	307
DB	1377	AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGGTGGCGACAGTCAAGAAGCAGCACT	1436
QY	308	GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln	327
DB	1437	GGAAAACTGTCAGCGCCCATGCGCTCGACACCATGTTCCAGTTAATGATCTCCCAAGCAA	1496
QY	328	LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTyrSerGluGlu	346
DB	1497	ATGTACGAGCACTTCAAGGGGTACAGATATGTCACAC---ATCACTGGAAGCAGAGAC	1553
QY	347	GlnAlaSerThrValLeuGlnAlaTyrGlnArgPheValGlnLeuAlaGlnGluAla	366
DB	1554	AAAGCGCAGCCCATCTGGAGGCTGGCAGAGGACATATGTGGAGGTGGTTTCATCAGAT	1613
QY	367	LeuProGluAsnAlaSerGlnIleHisAlaPheSerSerThrThrLeuAspAspIle	386
DB	1614	GTCCGACAGAACTCCATCAAAAGGTGCTTCTTCCACACAGCCCTCGGACGATC	1673
QY	387	LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu	406
DB	1674	CTGAATTCCTTCTGACGTGATGTCATCCGGTGGCCAGCGGCTACTTACTCATGCTC	1733
QY	407	AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly	426
DB	1734	GCCTATGCTGTCTAACCATGCTGCGCTGGGACTGCTGCCAAGTCCAGGGTGGCGTGGG	1793
QY	427	LeuAlaGlyValLeuLeuValAlaLeuAlaValAsnSerGlyLeuGlyLeuCysAlaLeu	446
DB	1794	CTGGCTGGCGCTCTGCTGTGCTGTCAGTGGCTGTCAGTGGCTGCGGCTGCTGCTCATG	1853
QY	447	LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle	466
DB	1854	ATCGGAATTCCTTAAACGCTGCACAACTCAGGTTTGGCAATTTCTCGCTCTTGGTGT	1913
QY	467	GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly-----	484

1914 GGTGTGGATGATGTTTCTTCTGCGCCACCGCTTCAGTGAACAGGACAGATAAAGA 1973
485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
1974 ATCCCTTTTGAGCAGACCGGGGAGTGCCTGAAGCGCACAGGAGCGGTGCGCTC 2033
505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
2034 ACGTCCATCAGCAATGTCACAGCTTCTTCATGGCGGCTTATCCCAATCCCCGCTCTG 2093
525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
2094 CGGGCGTCTCTCCCTCAGCGAGCGTAGTAGTGGTGTCAATTTTGGCCATGGTTCGTCTC 2153
545 ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal 564
2154 ATTTTCTGCTCAATCTCAGCATGATTTATATCGACGCGAGCAGAGACTGGATATT 2213
565 LeuCysCysPheSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
2214 TTCTGCTGTTTACAAAGCCCTCGCTCAGCAGAGTATTAGTTGAACCTCAGGCCTAC 2273
595 GlyAsp-----GlyThrValProValGlyIleAlaHis----- 595
2274 ACCGACACACAGCAATATCCCGCTACAGCCCCCACCCTCCCTACAGCAGCCACAGCTTT 2333
596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
2334 GCCCATGAACGCGAATTACCATCAGTCCACTGTCCAGCTCCGACGAGTACGACCCC 2393
609 SerSerGlnHisValValThrIleLeuProGlnAlaHisLeuValProProPro--- 627
2394 CACAGCAGCGTACTACACCACCGCTCAGCGCGCTCCCGAGATCTCTGTGCGACCCGTC 2453
628 -----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
2454 ACCGTGACACAGGACACCCCTCAGTGCAGAGCCAGAGCAGCAGCTCCACAAAGGAC 2513
645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
2514 CTGCTCTCCAGTGTCTCCGACTCC-----AGCTCCACTGCCTCGAGCCCCCTGTACG 2567
665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
2568 AAGTGGACATCTCATCTTTGCTGAGAAGCACTATGCTCTTCTCTTGAACCAAAA 2627
685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
2628 GCCAAGGTAGTGTGATCTTCTTTCTGGGCTTGCTGGGGGTACGCTTTATGGCACC 2687
705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHis 724
2688 ACCGAGTGAAGACGGGTGACCTTTACGACATTTGATCTCTCGGAAACAGAGAATAT 2747
725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
2748 GACTTTATTGCTGCACAAATCAATACTTTCTTCTACAAATGATATAGTACCCAG 2807
745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
2808 AAAGCA--GACTACCCGAATATCCAGCACTTACTTTAGACCTACACAGGAGTTTCAGT 2864
765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
2865 AAGCTGAAGTATGATCTGTTGGAGAAAAACAAACAGCTTCCCAAAATGTGGCTGCATAC 2924
785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
2925 TTCAGAGACTGGTTCAGGACTTCAGGATGCAATTTGACAGTACCTGGGAAACCGGAAA 2984
805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824

2985 ATCATGCCAAACAATTACAAGAAATGGATCAGAGATGGAGTCTTGCCTTACAAACTCTCG 3044
825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
3045 GTGCAAAACCGGCGAGCCGATAGCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG 3104
845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
3105 GTGGATGAGATGGCATTAATCCAGCGCTTTTCTACATCTACTCAGCGCTTGGGTC 3164
865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu 884
3165 AGCAAGACCCCGTCGCGTATGCTCTCCAGGCCAACATCCGCGCCACACCGACAGAA 3224
885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
3225 TGGTCCACGACAAAGCGGACTACATGCTGAAACAGGCTGAGAAATCCCGCAGCAGAG 3284
904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
3285 CCCATCAGTATGCCAGTTCCCTTTTACCTCAACGGGTTGCGGAGACACCTCAGACTTT 3344
924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
3345 GTGAGGCAATTGAAAGTAAGACCATCTGCAGCAACTATACGAGCCTCGGGCTGTCC 3404
944 AlaTyrProSerGlySerProPheLeuPheTyrGluGlnTyrLeuGlyLeuArgCys 963
3405 AGTTACCCCAACGCTACCTCTCTCTCTGAGGAGCAGTACATCGGCTCCGCGACTGG 3464
964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
3465 CTGTGTGTGTCATCAGCGTGTGTGGCTGCACATTCCTCGTGTGCGTGTCTCTT 3524
984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
3525 CTGAACCCCTGAGCGCGGATCATTTGATGCTCTGCGCTGATGAGCGTGCAGCTG 3584
1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
3585 TTGCGCATATGGGCTCTCGGAATCAAGCTAGTCCGCTGCGGCTGATCTCTGATC 3644
1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThr 1043
3645 GCTTCTGTGTCATAGAGTGGAGTTCACCGTTTTCAGCTTGTGGCTTTCGACGCGC 3704
1044 GlnGlySerArgAsnLeuArgAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
3705 ATCGGCGACAAAGAACCGGCTGTGCTTGGCCCTGAGCACAATGTTTGACCCGCTCTG 3764
1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
3765 GATGCGCGGTGTCCTTCTGTGTGCTGGCGATCTCTCACCATCTCGCGGCTTCTCAATGG 3824
1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuHisGly 1103
3825 ATTGTGAGTATTTCTTCTGTGTGCTGGCGATCTCTCACCATCTCGCGGCTTCTCAATGG 3884
1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal-IleGlnMe 1123
3885 CTGGTTTCTTCCCGTGTCTTGTCTTCTTGGACCATATCTCTGAGGTGTCTCCAGCC 3944
1123 tTyrLys-----GluSerProGluIleLeuSerProAlaProGlnGlyGln 1139
3945 AACGCGTTGAACCGCTGCCACACCTCCCTGAGCCACCCCGCGG----- 3993
1139 yGlyLeuArgTrpGlyAlaSerSerLeuProGlnSerPheAlaArgValThrSer 1159
3994 -----TGGTCCGCTTCGCCATGCCGCG-----GCCAC 4022
1159 rMetThrValAlaIleHisProPro----- 1167
4023 ACGCAGCGGCTCTGATTCTCCGACTCGGAGTATAGTTCCAGACAGACAGTGTGAGC 4082

Db 1614 GTCGCACAGAACTCCACTCAAAAGGTGCTTTCCTTACCACCAACGACCTGGACGACATC 1673
 Qy LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
 Db 1674 CTGAATCTCTCTGAGCTCAGTGTATCCGCGTGGCCAGCGGTACTTACTCATGCTC 1733
 Qy AlaTyrAlaCysValThrMetLeuArgTyrPheSerGluValSerGlnGlySerValGly 426
 Db 1734 GCCTATGCTGTCTAACCATGCTGGCTGGGACTGCTCCAGTCCAGGGTGGCGTGGGG 1793
 Qy LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
 Db 1794 CTGGCTGGCGTCTGCTGGTGTGCACTGTGAGTGGCTGAGGACTGGGCTGTGCTCATG 1853
 Qy LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
 Db 1854 ATCGAAATTTCTTTAAGCTGCAACCACTCAGGTTTGGCATTTCTCGCTCTTGGTGT 1913
 Qy GlyValAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly----- 484
 Db 1914 GGTGTGATGATGTTTCTTCTGCCCCAGCCTTCAGTGAACAGGACAGAAATAAAGA 1973
 Qy ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValLeu 504
 Db 1974 ATCCCTTTTGAGGACAGGACCGGGAGTGTGCTGAAGCGCACAGGAGCGGCTG 2033
 Qy ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
 Db 2034 ACCTCCATGCAATGTCACAGCCTTCTTCATGGCCGCGTTAATCCCAATTTCCCGCTCTG 2093
 Qy ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
 Db 2094 CGGCGGTTCCTCCAGGACGCGGTAGTAGTGTTCATTTTGGCCATGTTCTGCTC 2153
 Qy ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal 564
 Db 2154 ATTTCCTCCAAATCTTCACATGATTTATATCGACGCGGACAGGAGACTGGATAT 2213
 Qy LeuCysCysPheSerProCysSerAlaGluValIleGlnIleLeuProGlnGluLeu 584
 Db 2214 TTCTGTGTTTTCAGACCCCTCGCTCAGCAGAGTGAATCAGGTTGAACCTCAGGCTAC 2273
 Qy GlyAsp-----GlyThrValProValGlyIleAlaHis----- 595
 Db 2274 ACCGACACACACGACAAATCCCGCTACAGCCCCCCTCCCTCCACAGCAGCCACGCTT 2333
 Qy 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
 Db 2334 GCCCATGAACGACAGATTACCATGCACTGCTCAGCTCCGCGCAGGAGTACGACCCC 2393
 Qy 609 SerSerGlnHisValThrIleLeuProProGlnAlaHisLeuValProPro----- 627
 Db 2394 CACACGCGTGTACTACACCCGCTGAGCGCGCTCCGAGATCTCTGTGACGCGCCGTC 2453
 Qy 628 -----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
 Db 2454 ACCGTGACACAGGACACCCCTCAGCTCCAGAGCCGACAGAGACACAGTCCACAGGGAC 2513
 Qy 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
 Db 2514 CTGCTCTCCAGTCTCTCCGACTCC-----AGCCTCCACTGCTCCGAGCCCTGTACG 2567
 Qy 665 ArgTyrAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
 Db 2568 AGTGAGACTCTCATCTTTGCTGAGAAGCACTATGCTCTTCCTTGTGAACCAAAAA 2627
 Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
 Db 2628 GCCAAGTAGTGTGATCTCTTTTCTGGGCTGCTGGGGTACGCTTTTATGGACCC 2687
 Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHis 724
 Db 2688 ACCCGAGTGAGAGACGGGTGACCTTACGGACATTTGTACCTTCGGGAAACAGAGATAT 2747

Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
 Db 2748 GACTTTATTTGTCGACAAATTCAAATACTTTTCTTTTACAAATGATATATAGTACCCAG 2807
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 Db 2865 AACGTGAAGTATGTCATGTTGGAAGAAACAAACAGGTTCCCAAAATGTGGCTGCACATC 2924
 Qy 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
 Db 2925 TTCAGAGACTGGCTTCAGGACTTCAGGATGCAATTCAGAGTGAAGTGGGAAACCGGAAA 2984
 Qy 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
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 Qy 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
 Db 3045 GTGCAACCGCGACCGCGGATAGCCCATCGACATCGACAGTGTGACTAAACAGCGTGTG 3104
 Qy 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
 Db 3105 GTGGATGTCAGATGGCATTAATCCAGCGCTTCTTACATCTACCTGACGGCTGGGTC 3164
 Qy 865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu 884
 Db 3165 AGCAACGACCCCGTGGGTATGCTGCTCCAGGCCCAACATCCGGGCCACACCGACAGAA 3224
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 Qy 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
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 Qy 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
 Db 3345 GTGAGGCAATTTGAAAGAAAGTAAAGGACCATCTGCAGCAACTATACGAGCCTGGGCTGTC 3404
 Qy 944 AlaTyrProSerGlySerProPheLeuPheTyrGluGlnTyrLeuGlyLeuArgCys 963
 Db 3405 AGTTACCCCAACGGCTACCCCTTCTCTTCTGGGACAGTACATCGGCTCCGCCACTGG 3464
 Qy 964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeu 983
 Db 3465 CTGCTGCTCTTCATCAGCGTGTGGCTGCACATTCTCGTGTGCTGCTTCTTCTT 3524
 Qy 984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
 Db 3525 CTGAACCCCTGACGCGCGGATCATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3584
 Qy 1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
 Db 3585 TTCGCGCATGATGGCTCATCGGAATCAAGCTCAGTCCGCTGCTGCTGCTGCTGCTGCT 3644
 Qy 1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThr 1043
 Db 3645 GCTTCTGTGGCATAGGAGTGGAGTTCACCGTTCAGTGTGCTTTCGCTTCTGACGGCC 3704
 Qy 1044 GlnGlySerArgAsnLeuArgAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
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 Qy 1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
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QY 1084 lleValArgTyrPhePheAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
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QY 1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal-IleGlnMe 1123
Db 3885 CTGGTTTGTCTCCCGTCTTTGTTCTTTCTTGGACCATATCTGAGGTGTCTCAGCC 3944
QY 1123 tTyrLys-----GluSerProGluLeuLeuSerProProAlaProGlnGly 1139
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QY 1139 yGlyLeuArgTyrGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrSe 1159
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QY 1159 rMetThrValAlaIleHisProPro----- 1167
Db 4023 ACCCAGCGGGTCTGATTCCTCGACTCGAGTATAGTTCCAGACGACAGTGTGACGC 4082
QY 1168 -----ProLeuProGlyAlaTyrIleHisProAlaProaspG 1180
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QY 1180 uProProTrpSerProAlaAlaThrSerSer 1190
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RESULT 12
US-08-918-658-18
; Sequence 18, Application US/08918658
; Patent No. 6429354
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; ;
; ; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,658
; FILING DATE: 22-Aug-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/656,055
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-918-658-18
Alignment Scores:
Pred. No.: 2,75e-304 Length: 5288
Score: 3349.00 Matches: 662
Percent Similarity: 70.02% Conservative: 200
Best Local Similarity: 53.78% Mismatches: 298
Query Match: 53.40% Indels: 71
DB: 16
US-09-990-046-2 (1-1203) x US-08-918-658-18 (1-5288)
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Db 540 CCCAGCTACTGC---GACGCCGCTTCGCTCTGGACAGATTTCCAGGGGAAGGCTACT 596
QY 31 -----LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly 48
Db 597 GCGCGGAAAGCGCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTAAACTGGGT 656
QY 49 CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuAlaPheGlyAla 68
Db 657 TGTTCATTCAAAAAAAGTCCGCAAGTTCCTGGTTGTGGGCTCTCTCATATTGGGGGCC 716
QY 69 LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu 88
Db 717 TTCGCGTGGGATTAAGCAGCGAAGCTCGAACCAACGCTGGAGGAGCTTGGGTGAA 776
QY 89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGlnLysLeuGlyGluAla 108
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QY 109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGluAsnIleLeuThr 128
Db 837 ATGTTTAATCCTCAACTCATGATACAGACCCCTAAAGAGAGAGTGTGTAATGCTCTACC 896
QY 129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
Db 897 ACAGAGCGCTCTCTACACACTTGGACTCGGCACTCCAGGCCAGCGCTGCTCATGTATAC 956
QY 149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db 957 ATGTACAAACAGGAGTGGAAATTTGGAACATTTGTGTATACAAATCAGAGAGCTTATCACA 1016
QY 169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuThrPro 188
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QY 229 ---AlaSerLeuGluGlyPheArgGluLeuAspLysAlaGlnValGlnAlaTyr 247
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QY 248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis 267
Db 1257 ATGGACCGCCCTCGCTCAATCCGCGCGATCCAGACTGCCCGCCAGCCCAACAAA 1316
QY 268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyCysHisGlyPheSer 287
Db 1317 AATTCAACCAACCTCTTTGATATGGCCCTTTGTTGAATGGTGGATGTCATGGCTTATCC 1376
QY 288 HisLysPheMetHisTrpGlnGluLeuLeuLeuGlyMetAlaArgAspProGln 307
Db 1377 AGAAGTATATGCACTGGCAGGAGGATTTGATTGTGGGTGGCAGTCAAGAACAGCACT 1436

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308	Gly	Glu	Leu	Leu	Arg	Ala	Glu	Ala	Leu	Gln	Ser	Thr	Phe	Leu	Leu	Met	Ser	Pro	Arg	Gln	327
1437	GGAAAACTCGT	CAGCGCC	CGCTG	CAGCAG	CGCTG	CAGCAG	CGCTG	TTC	CAGT	TTT	CAGT	TTT	TAAT	GACT	ACCT	CCCAAG	CAA	1456			
328	Leu	Tyr	Glu	His	Phe	Arg	Gly	---	Asp	Tyr	Gln	Thr	His	Asp	Leu	Gly	Trp	Ser	Glu	Glu	346
1497	ATGTAAGAGCACTT	CAAGGGG	TAC	GAGT	ATG	TCT	CAC	AC	---	ATC	AACT	TGA	AC	CAG	CGAC	1553					
347	Gln	Ala	Ser	Thr	Val	Leu	Gln	Ala	Trp	Gln	Arg	Arg	Phe	Val	Gln	Leu	Ala	Gln	Ala	366	
1554	AAAGCGG	CAGC	CACT	CTCG	AGSCCT	TGG	CAG	AGG	CA	TAT	TGG	AGG	TGG	TT	CAT	CAG	AGT	1613			
367	Leu	Pro	Glu	Asn	Ala	Ser	Gln	Gln	Ile	His	Ala	Phe	Ser	Ser	Thr	Thr	Leu	Asp	Asp	386	
1614	GTGCGAC	AGAACT	CTC	ACT	CAAAAG	TGCT	TCT	CC	TTC	AC	CA	CGA	CCG	AC	CGA	CCG	TGG	AC	GAT	1673	
387	Leu	His	Ala	Phe	Ser	Glu	Val	Ser	Ala	Ala	Arg	Val	Val	Gly	Gly	Tyr	Leu	Leu	Met	406	
1674	CTGAAT	CTCTT	CT	CTG	AGCT	CAG	TGT	CAT	CCG	GTG	GC	AG	CGG	CT	ACT	TACT	TACT	CAT	CTC	1733	
407	Ala	Tyr	Ala	Cys	Val	Thr	Met	Leu	Arg	Trp	Asp	Cys	Ala	Gln	Ser	Gln	Gly	Ser	Val	Gly	426
1734	GCCTAT	GCCT	GCT	GCT	TAAC	CACT	CT	GG	CT	GG	ACT	GCT	CC	AG	TCC	AG	GGT	CG	CT	GGG	1793
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1794	CTGGCT	GGCG	TC	CT	GGT	TG	CACT	TG	CA	TG	CT	GC	AG	TCC	AG	GGT	CG	CT	GGG	1793	
447	Leu	Gly	Ile	Thr	Phe	Asn	Ala	Ala	Thr	Gln	Val	Leu	Pro	Phe	Leu	Ala	Leu	Gly	Ile	466	
1854	ATCGGA	ATTTC	TTT	TAAC	GC	TGC	AA	CACT	CAG	GT	TTT	TG	CA	TCT	TC	CG	CT	TCT	GT	GT	1913
467	Gly	Val	Asp	Asp	Val	Phe	Leu	Leu	Ala	His	Ala	Phe	Thr	Glu	Ala	Leu	Pro	Gly	---	484	
1914	GGTGTG	ATG	ATG	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	484
485	Thr	Pro	Leu	Gln	Glu	Arg	Met	Gly	Glu	Cys	Leu	Gln	Arg	Thr	Gly	Thr	Ser	Val	Val	Leu	504
1974	ATCCCT	TTT	TG	AG	CAG	AG	CG	AG	TG	CT	GA	AG	CG	CA	CG	AG	CG	CA	CG	CG	2033
505	Thr	Ser	Ile	Asn	Asn	Met	Ala	Ala	Phe	Leu	Met	Ala	Ala	Leu	Val	Pro	Ile	Pro	Ala	Leu	524
2034	ACGTCC	AT	CAG	CAAT	GT	C	AG	CA	CTT	CTT	CAT	G	CG	CG	CGT	TAAT	CCCAAT	TC	CG	CT	2093
525	Arg	Ala	Phe	Ser	Leu	Gln	Ala	Ala	Ile	Val	Val	Gly	Cys	Thr	Phe	Val	Ala	Val	Met	Leu	544
2094	CGGCGG	TTCT	CCCT	CC	AG	CG	CG	G	TAG	TAG	TGG	TGT	TCA	ATT	TTG	CC	AT	TGT	CT	CT	2153
545	Val	Phe	Pro	Ala	Ile	Leu	Ser	Leu	Asp	Leu	Arg	Arg	Arg	His	s	Cys	Gln	Arg	Leu	Asp	564
2154	ATTTT	TTCT	CG	CAAT	CT	CAG	CT	GG	AT	TAT	TAT	CG	CG	CG	CG	CG	CG	CG	CG	CG	2213
565	Leu	Cys	Cys	Phe	Ser	Ser	Pro	Cys	Ser	Ala	Gln	Val	Ile	Gln	Ile	Leu	Pro	Gln	Glu	Leu	584
2214	TTCTGT	GT	TTT	TAC	AG	CCCT	CG	TC	AG	CAG	AGT	GAT	T	CAG	GT	GAA	CT	CAG	CG	CT	2273
585	Gly	Asp	---																		

Db	2514	CTGCTCTCCAGTTCCTCGACTCC-----AGCCTCCACTGCCTCGAGCCCCCTGTACG	2567
Qy	665	ArgTrpAsnLeuAlaHisPheAlaAargTyrGlnPheAlaProLeuLeuGlnSerHis	684
Db	2568	AAGTGGACACTCTCATCTTTTGGCTGAGAAGCACTATGCTCTCTCTTGAACCAAAA	2622
Qy	685	AlaLysAlaIleValLeuValPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla	704
Db	2628	GCCAAAGTAGTGGTATCTTCTTTTCTGGGCTGTCTGGGGTCAACCTTTATGGCACC	2687
Qy	705	ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProAargGlyThrLysGluHis	724
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Qy	725	AlaPheLeuSerAlaGlnLeuAargTyrPheSerLeuTyrGluValAlaLeuValThrGln	744
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Qy	745	GlyGlyPheAspTyrAlaHisSerGlnAargAlaLeuPheAspLeuHisGlnAargPheSer	764
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Qy	765	SerLeuLysAlaValLeuProProAlaThrGlnAlaProAargThrTyrLeuHisTyr	784
Db	2865	AACGTGAAGTATGTCATGTTTGGAGAAAAACAACAGCTTCCAAAATGTGGCTGCATC	2924
Qy	785	TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg	804
Db	2925	TTACAGACACTGGCTTTCAGGACCTTCAGATGTCAATTTGACAGTCACTGGGAAACCGG	2984
Qy	805	IleThrArgHisSerTyrAargAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu	824
Db	2985	ATCATGCCAAACAATACAAAGATGGATCAGACATGGAGTCTTGCTTCAAACTCCTG	3044
Qy	825	IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrAargLysLeu	844
Db	3045	GTGCAAAACCCGACGCGCGATAAGCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG	3104
Qy	845	ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal	864
Db	3105	GTGGATGCAGATGGCATTAATCCCGAGCGCTTTCTACATCTACCTGACGGCTTGGTC	3164
Qy	865	SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu	884
Db	3165	AGCAACGACCCCGTCGGCTATGCTGCTCCAGGCCAACATCCGGCCACACCGACAGAA	3224
Qy	885	TrpLeuHisAspLysTyrAspThrThrGlyGlu--AsnLeuArgIleProProAlaGln	903
Db	3225	TGGGTCCACGACAAAGCCGACTACATCGCTGMAACAAGCTCGAGAAATCCGGCAGCAGAG	3284
Qy	904	ProLeuGluPheAlaGlnPheProPheLeuLeuAargGlyLeuGlnLysThrAlaAspPhe	923
Db	3285	CCCATCGATGCCAGATTCCTTTCTACCTCAACGGGTTCGGGACACCTCAGACTTT	3344
Qy	924	ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis	943
Db	3345	GTGAGGCAATTGAAAAGTAGGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC	3404
Qy	944	AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuAargArgCys	963
Db	3405	AGTTACCCCAACGGCTACCCCTTCTCTTCTGGGAGCAGTACATCGGCTCCGCCACTGG	3464
Qy	964	PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu	983
Db	3465	CTGCTCTCTTATCATAGCGTGTGTGGCTTCACATTCCTCGTGTGGCTGTCTTCCTT	3524
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Qy	1004	PheGlyIleMetGlyPhePheGlyIleLysLeuSerAlaIleProValIleLeuVal	1023

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QY 328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
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QY 347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgPheValGlnLeuAlaGlnGluAla 366
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1554 AAAGCGGACCATCTCGAGGCGCTGGCAGAGGACATATGTGGAGGTGGTTTCATCAGAGT 1613
QY 367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspIle 386
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1614 GTCGCACAACTCCACTCAAAAGGTGCTTCTCCACCACGACGACCCCTGGACGACATC 1673
QY 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db
1674 CTGAAATCTTCTTCAGCTGCTGTCAGTCCCGGTGGCCAGCGCTACTTACTCATGCTC 1733
QY 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
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1734 GCCTATGCTGCTTAACCATGCTGCGCTGGAGTCTCCAAAGTCCCGAGGTGCGGGGG 1793
QY 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db
1794 CTGGCTGGCGTCTGCTGGTTCAGCTGCTGAGTGGCTGAGGCTGCGGCTGCTGCTCATG 1853
QY 447 LeuGlyIleThrPheAsnAlaAlaThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db
1854 ATCGGAATTCCTTTAACTGCTCAACTCAGTTTTCCTGCTTCTGCTGTT 1913
QY 467 GlyValAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly----- 484
Db
1914 GGTGTGGATGATGTTTTCTTCTGCCCCACGCTTCAGTGAACAGGACAGAAATAAAGA 1973
QY 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db
1974 ATCCCTTTTGAGGACAGGACCGGGAGTGCCTGAAGCGCACAGGACCGCTGCGCTC 2033
QY 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
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2034 AGTCCATCAGCAATGTCACAGCTTCTTCACTGGCGGCTTAATCCCAATTCCTGCTG 2093
QY 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
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QY 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal 564
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596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
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2334 GCCATGAAACGAGATTACCATGTCCACTGTCCAGCTCCGACGGAGTAGCAGCCCC 2393
QY 609 SerSerGlnHisValValThrIleLeuProGlnAlaHisLeuValProPro--- 627
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2394 CACACGACGTGTACTACACCCGCTGAGCGCGCTCCGAGATCTCTGTGACGCCGTC 2453
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QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
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QY 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
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2628 GCCAAGGTAGTGTGATCTCTTTTCGGGCTTCTCGGGGTGAGCTTTATGGCACC 2687
QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
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2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTACGACTACAGGAGTTTCACT 2864
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QY 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
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3165 AGCAACGACCCCGTCGCTATGCTCCAGGCGCAACATCCGCGCACACGACGACGAG 3224
QY 885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
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QY 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
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QY 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
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Db 1077 TTGGACTGCTTCTGGGAAGGGCGAAATTAACAGTCTGGGACAGCATACCTCTAGGTAAA 1136
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Db 1137 CCTCTTTGGGTGGCAAACTTCGACCCCTTGGAAATTCCTGGGAAGAGTTAAAGAAATA 1196
QY 229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr 247
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QY 248 ValGlyArgProCysLeuHisProAspAspLeuHisCysProSerAlaProAsnHis 267
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RESULT 15

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PCT-US95-13233-18
; Sequence 18, Application PC/TUS9513233
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF TRUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
```

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; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13233
; FILING DATE: 06-OCT-1990
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-13233-18
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Alignment Scores: 2.75e-304 Length: 5288
Pred. No.: 3349.00 Matches: 662
Score: 3349.00 Conservative: 200
Percent Similarity: 70.02% Mismatches: 298
Best Local Similarity: 53.78% Indels: 71
Query Match: 53.40% Gaps: 16
DB: 5
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US-09-990-046-2 (1-1203) x PCT-US95-13233-18 (1-5288)

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Sun Nov 28 09:38:31 2004

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 07:58:50 ; Search time 7917 Seconds
(without alignments)
7185.741 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

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Ygapop 10.0 , Ygapext 0.5
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Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	6272	100.0	3765	9 AY359016 Homo sapi
4	6272	100.0	4030	6 BD194644 Vertebrat

5	6272	100.0	4030	6	AR194379	Sequence
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9	6229	99.3	3612	9	AF087651	Homo sapi
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19	4042.5	64.5	3672	5	DRPATCH	X96883 D. rerio mRN
20	3991.5	63.6	170141	2	AL611928	Homo sapi
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VERSION	AF091501.1	GI:3929234			
KEYWORDS					
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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 3612) Frantz, G., Rosenthal, A., and de Sauvage, F.J., Carpenter, D., Stone, D.M., Brush, J., Ryan, A., Armanini, M., Characterization of two patched receptors for the vertebrate hedgehog protein family				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 95 (23), 13630-13634 (1998)				
MEDLINE	99030620				
PUBMED	9811851				
REFERENCE	2 (bases 1 to 3612) de Sauvage, F.J., and Carpenter, D.				
AUTHORS	Direct Submission				
TITLE	Submitted (11-SEP-1998) Molecular Oncology, Genentech Inc, 1 DNA				
JOURNAL	Way, So. San Francisco, CA 94080, USA				
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Query Match: 100.00% Indels: 0
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US-09-990-046-2 (1-1203) x AF091501 (1-3612)

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LOCUS

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Homo sapiens clone DNA35621 Patched 2 (UNQ560) mRNA, complete cds.

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VERSION	AY358555.1	GI:37182232	
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ORGANISM	Homo sapiens		
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TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment		
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)		
PUBMED	12975309		
REFERENCE	2 (bases 1 to 3641)		
AUTHORS	Clark,H.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
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AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
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Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
PUBMED 12975309
REFERENCE 2 (bases 1 to 3765)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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JOURNAL Patent: US 6348575-A 1 19-FEB-2002;

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Db	293	GCAGCACCCAGATCTAGCTGGAGCCTGAAGCTCCACTCTGGCTTCGTGCTTACTTC	352
QY	41	GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe	60
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ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 4030)
AUTHORS   de Sauvage, F. and Carpenter, D.A.
TITLE      Nucleic acid encoding patched-2
JOURNAL    Patent: US 6709838-A 1 23-MAR-2004;
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Percent Similarity: 100.00%      Conservative: 0
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Query Match:      100.00%      Indels:      0
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QY |||||
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ACCESSION AR374936
VERSION AR374936.1 GI:40078100
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4391)
AUTHORS Bumcrot,D.A.
TITLE Human patched genes and proteins, and uses related thereto
JOURNAL Patent: US 6605700-A 1 12-AUG-2003;
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Query Match: 99.62% Indels: 0
DB: 6 Gaps: 0

US-09-990-046-2 (1-1203) x AR374936 (1-4391)

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361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
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 VERSION AF087651.1 GI:4588014
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (Bases 1 to 3612)

AUTHORS Smyth, I., Narang, M.A., Evans, T., Heimann, C., Nakamura, Y.,
Chenevix-Trench, G., Pietsch, T., Wicking, C. and Wainwright, B.J.
Isolation and characterization of human patched 2 (PTCH2), a
putative tumour suppressor gene in basal cell carcinoma and
medulloblastoma on chromosome 1p32
Hum. Mol. Genet. 8 (2), 291-297 (1999)
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9913336
2 (bases 1 to 3612)
Smyth, I., Narang, M.A., Evans, T., Heimann, C., Nakamura, Y.,
Chenevix-Trench, G., Pietsch, T., Wicking, C. and Wainwright, B.J.
Direct Submission
Submitted (28-AUG-1998) Center for Molecular and Cellular Biology,
University of Queensland, Ritchie Laboratories, Research Rd.,
Brisbane, QLD 4072, Australia
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FEATURES

source

gene

CDS

ORIGIN

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US-09-990-046-2 (1-1203) x AF087651 (1-3612)

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3453)
 AUTHORS Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and Toftgard,R.
 TITLE PTCH2, a novel human patched gene, undergoing alternative splicing and up-regulated in basal cell carcinomas
 JOURNAL Cancer Res. 59 (4), 787-792 (1999)
 MEDLINE 99151521
 PUBMED 10029063
 REFERENCE 2 (bases 1 to 3453)
 AUTHORS Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and Toftgard,R.
 TITLE Direct Submission
 JOURNAL Submitted (12-JAN-1999) Bioscience, Karolinska, Huddinge 141 57, Sweden

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gene
 CDS

ORIGIN

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Db	1513	AGTGTGCTACTCACATCCATCAACAACATGGCGCCCTTCTCATGTGCTGCGCTCTGCC	1572
QY	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540
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QY	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560
Db	1633	GCGGTGATGCTTGTCTTCCAGCATCTCCAGCTGGACCTACGGCGGCGCCACTGCCAG	1692
QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
Db	1693	CGCCTTGATGTCTCTGTGCTTCTCCAGTCCCTGTCTGTCTCAGTGATTCAGATCCTG	1752
QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
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QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
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QY	621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
Db	1873	GCCCACTGGTGGTGGCCCACTTCTGACCCACATGGGCTCTGAGCTCTTACGCCCTGGAGG	1932
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QY	661	LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
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QY	681	LeuGlnSerHisAlaIysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700
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QY	701	LeuTyrGlyAlaThrIleuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly	720
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QY	721	ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740
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SOURCE   Mus musculus (house mouse)
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REFERENCE
AUTHORS Takabatake,T., Ogawa,M., Takahashi,T.C., Mizuno,M., Okamoto,M. and Takeshima,K.
TITLE    Hedgehog and patched gene expression in adult ocular tissues
JOURNAL FEBS Lett. 410 (2-3), 485-489 (1997)
MEDLINE 97379366
PUBMED  9237688
REFERENCE
AUTHORS Motoyama,J., Takabatake,T., Takeshima,K. and Hui,C.
TITLE    Ptch2, a second mouse Patched gene is co-expressed with Sonic hedgehog
JOURNAL Nat. Genet. 18 (2), 104-106 (1998)
MEDLINE 98122566
PUBMED  9462734
REFERENCE
AUTHORS Takabatake,T.
TITLE    Direct Submission
JOURNAL Submitted (04-FEB-1998) Takashi Takabatake, Nagoya University, Radioisotope Research Center, Furo-cho, Chikusa, Nagoya, Aichi 464-8602, Japan (E-mail:j45998@nucc.cc.nagoya-u.ac.jp, Tel:052-789-2573, Fax:052-789-2567)
COMMENT On Feb 6, 1998 this sequence version replaced gi:2598660.
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            YKSGVPLIENGMIETRMIEKLPFCVILTLPDPCFWEGAKLQGSAYLFPERDIOETNLDP
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ORIGIN

Alignment Scores:

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Percent Similarity: 94.58%      Conservative: 43
Best Local Similarity: 90.94%      Mismatches: 64
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US-09-990-046-2 (1-1203) x AB010833 (1-3549)

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 partial cds.

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 KEYWORDS
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 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4402)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Udín,T.B., Toshiyuki,S., Abramson,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J., Carrington,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzyzanski,M.I., Skalska,U., Smalley,D.E., Gnererich,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 4402)
 Direct Submission
 Strausberg,R.
 Submitted (16-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
 Parvaneh Saeedi, JR Santos, Angeliue Schnerch, Ursula Skalska,
 Duane Smalley, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 126 Row: o Column: 8
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6679516.

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US-09-990-046-2 (1-1203) x BC058397 (1-4402)

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DEFINITION Sequence 3079 from Patent WO02068579.
ACCESSION CQ717145
VERSION CQ717145.1 GI:42278002
KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 3079 06-SEP-2002;
PE Corporation (NY) (US)
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DEFINITION Novel constitutional elements in hedgehog transmission pathway.
ACCESSION BD227644
VERSION BD227644.1 GI:33037414
KEYWORDS JP 2002526050-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12886)
AUTHORS Zaphiropoulos, P.G., Unden, A.B., Toftgard, R., Rahnama, F. and Hollingsworth, R.E.
TITLE Patent: JP 2002526050-A 4 20-AUG-2002;
JOURNAL KAROLINSKA INNOVATIONS AB, PHARMACIA AND UPJOHN CO
COMMENT OS Homo sapiens (human)
PN JP 2002526050-A/4
PD 20-AUG-2002
PF 06-OCT-1999 JP 2000573395
PR 06-OCT-1998 SE 9803393-9
PI PETER G ZAPHIROPOULOS, ANNE BIRGITTE UNDEN, RUNE TOFTGARD, PI FAHIMEH RAHNAMA,
PI ROBERT E HOLLINGSWORTH

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Db 1587 GCTTCTCCACTTCCCTGGCAGAGCTCCAGGAGCCAGAAAGCTGGGAGTGGGCTGGGCC 1646
QY 88 88
Db 1647 ATGACGAGGCCCTCAGGATAGAGGAGGAGGACTCTCTCTGCGCAGCTCTCCCACTTGT 1706
QY 88 88
Db 1707 TGGGAGGCGCTCAGAGTTAGAGGCCCTTTCGCAAGTTCTGACCCGCTAGGCCCTTTCC 1766
QY 89 89
Db 1767 CCCCCAGCTTTCTCTGTTTCTGCTTCTGGCAGTGGGCGCGGGTGGAGCCAGGAGCTGCATTA 1826

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QY 99 rThrLysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAl 119
Db 1827 CACCAAGGAGAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCG 1886
QY 119 aArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAl 139
Db 1887 ACGCCAGGAGGAGAGAACTCTCACACCGAAGCACTTGGCCCTCCACCTCCAGGCGAGC 1946
QY 139 aLeuThrAlaSerIysValGlnValSerLeuTyrGlyLysSer----- 153
Db 1947 CCTCACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGGT-GAGTCTGGCTGAGCCCC 2005
QY 153 ----- 153
Db 2006 TGAGCAGCTGGGGCGGAGCGTGTGTGGGGTTCGGAGTGGGAATCCCTCTTCTCTGC 2065
QY 154 -----TrrAspLeuAsnLysIleCysTyrIysSe 163
Db 2066 TGATCTCTATGCCCCCTGGCTATTGCAGTCTCTGGATTTCGAACAAATCTGCTACAAGTC 2125
QY 163 rGlyValProLeuIleGluAsnGlyMetIleGlu----- 174
Db 2126 AGGAGTTCCTCTTATTGAAATGGAATGATTGAGCGGTAAGTGTCTCTGAGAGGAGTAG 2185
QY 174 ----- 174
Db 2186 AGGCAGAACTTTTCTGTAGCTGGGAGGACTCAGAGACCGAGCAAGCCCCACAGCGCTGC 2245
QY 174 ----- 174
Db 2246 AATCTGCCCCCTTAAAACTAAGAGGGGATTGACAGAGGSCATCTACAAAGTTGTGGG 2305
QY 175 -----Trr-----MetIleGluLysLeuPheProCysVa 184
Db 2306 GCAGAGCTGACGCGGGGCGCGGATCCCTGGCAGATGATTGAGAAGCTGTTTCCGTGCGT 2365
QY 184 lIleLeuThrProLeuAspCysPheTrrGluGlyAlaLysLeuGlnGlyClySerAlaTy 204
Db 2366 GATCTCACTCCCTCTGACTGTCTTCTGGAGGGAGCCAACTCCAAGGGGGTCCCGCCTA 2425
QY 204 rLeuProGly----- 207
Db 2426 CCTGCGGTG-AGTGCCACTCTCTGGGSCCTGCTTCATCTCCGCTGGGACTCTCCAGC 2484
QY 207 ----- 207
Db 2485 AGAAAGGAGGCTCTGGGAATGAGGATGATCAAACTTACCAAGGTCTTAATTACCTC 2544
QY 207 ----- 207
Db 2545 CCAGGCCAGAACAGAGACATGGGCTTCCCAAGGCTCTTCCACATCTCTCTCTCTT 2604
QY 207 ----- 207
Db 2605 TCCCTCTCAAGGAAGAGACCTGACTATTATTACAAAACCTAAACACAAAGATCTGTAA 2664
QY 207 ----- 207
Db 2665 GATCTGAGCAAGAGAGAAAAAGATCCCCAAGAGGCTTTGCTGGGGAAATTAACCTAG 2724
QY 207 ----- 207
Db 2725 GTGTTTGCTAACCATTGCCAGGCGCAGAAAGAAACCTGTACAGGCGATGTGCTGTG 2784
QY 207 ----- 207
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QY 207 ----- 207
Db 2845 CTTTCTATGTATTAGTTAAACCTGCCCTGATATCGTCTCAGCCCCCTTGTACTCTTCTAC 2904

QY 207 ----- 207
Db 2905 AGCTCACTGTAGCACCCCTGGTGGGCCCATGAGCCTGGCAGTTCTGAGAAGCTGAGGCTT 2964
QY 207 ----- 207
Db 2965 GCACACCCCTCCATATGGAAGGACAAATCGGCAGATAGAGGAGGGTGGGTACAGCATGG 3024
QY 207 ----- 207
Db 3025 CGCCCCAGCAGCAGTGTGGAGCCCTGGTGTTCGTCCCTGACCCCTCACCAACTATAGGCTT 3084
QY 208 -----ArgProAspIleGlnTrrPthrAsnLeuAspProGluGlnLeuL 223
Db 3085 TTCCCTCAGCGCGCGCCGGATATCCAGTGGACCAACTGGATCCAGCAGCAGCTGTCTGA 3144
QY 223 uGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLysIleGlnVa 243
Db 3145 GGAGCTGGGTCCCTTTGCCCTCCCTTGGGCTTCCGGAGCTCTAGACAAGGCACAGGT 3204
QY 243 lGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCysProProSe 263
Db 3205 GGCCAGGCGCTACGTGGGCGGCGCTGTCTGCACCTGTATGACTCCACTGCCCACTAG 3264
QY 263 rAlaProAsnHisHisSerArg----- 270
Db 3265 TGCCCCCAACCATCACAGCAGCGAGTGGGTTCAAACACAGGTCTGCCAGGAAAGGCTGT 3324
QY 270 ----- 270
Db 3325 TTTCCTTCCCTTTCCTTCTCTCACTCTCTGTGTTCTGGGGAGAGTGAAGTCTGTGTGCC 3384
QY 270 ----- 270
Db 3385 CTGACCCCGCACTTCTCTGCCATTTATACCTGCTCCACAGTGCAGCGCCCCCAATGTT 3444
QY 270 ----- 270
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QY 270 ----- 270
Db 3505 TTTCCTAAGCTAGATAAGCTGGAAGTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 3564
QY 270 ----- 270
Db 3565 ACCCAGGCTGAGTGCAGTGTTCGATCTTGCTCACTGCAACCTCGGCTCAGCAATTC 3624
QY 270 ----- 270
Db 3625 TCTGCTTTAGCTCTCTGAGTAGTGGGATTACAGTGGCCACCACCATGCCCCGCTAAT 3684
QY 270 ----- 270
Db 3685 TTTTATTAGCTCCCAAAAGTGTGGGATTACAGGCGTGAAGCACTGCGCTGGCCAAAGSC 3744
QY 270 ----- 270
Db 3745 TGGACTTTTATCAAAATAGACTAATACAGGGAAACTAAGBAACACAGCAGGTAAAGCATGA 3804
QY 270 ----- 270
Db 3805 ATATCATACCTGGTTTCCAGGTTTCTTTGTGGCCCTGCAAAATGTGGTACTTTTTTTCAGA 3864
QY 270 ----- 270
Db 3865 ATCCGCCAGTTACACCAGCTCTCTCCAGAACCTACTTCCAGGCGCTGTCTTCCCTTTGG 3924
QY 270 ----- 270
Db 3925 GGCCTTCTGTCTGGGGATACCTAGTGTCTCACTCTCGAGAGCAGTCAAGAGGCTCAGAA 3984
QY 270 ----- 270

Db	3985	TAGTTACCTACACTCCAGCCCTACTGAGCTTCATGCGACGGTGGTTCTCTGGAGGTGAAG	4044	Db	5063	CAGGTGCTGCCCTTCTTGCTCTGGGAATCGCGGTGGATGACGTATTCTCTGCTGGCGCAT	5122
QY	270	-----	270	QY	477	AlaPheThrGluAlaLeuProGlyThrProLeu	487
Db	4045	CCAGGGACACTCAGTTATCCACGGCCAGGGCCTTGAGCATTAACCCCTCTCTGTTCCCT	4104	Db	5123	GCTTCACAGAGGCTCTGCTTGGCACCCCTCTCCAGGTGGGCCCTTGTCCTCCACAGGGCTC	5182
QY	271	-Gln-AlaProAsnVallAlaHisGluLeuSerGlyCysHisGlyPheSerHisLysP	290	QY	487	-----	487
Db	4105	CCAGGGCTCCCAATGTGGCTCAGAGCTGAGTGGGGCTGGCCATGGCTTCTCCCAAAAT	4164	Db	5183	ATCTGAGGAGCTCAGCTTACTGGTTAAGAGCCTCTTGTTCAAGTGAACCTTTGGGCTGC	5242
QY	290	heMetHisTrpGlnGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluL	310	QY	487	-----	487
Db	4165	TCATGCACTGGCAGGAGGAATTGCTCTGGAGGCATGCCAGAGACCCCCAGGAGAC	4224	Db	5243	TAATGAACCTCGTGCTTCTGTCCTCCCATCTCTAAACAGGGGAAATAATAGTGTGTGTC	5302
QY	310	euLeu	311	QY	487	-----	487
Db	4225	TGCTGAGGTAGGTCTCCTCTGGGAGTTGGTGAGGGGACTCTGTTTCATGAGAACCCTATC	4284	Db	5303	CTAAGGTTAATGTTTGGATCAGTGAGGTAACTCAAGTTGAATGCTTAGAACAGCCCATC	5362
QY	311	-----	311	QY	487	-----	487
Db	4285	TGTAATGCCAGGAGCTCTGGCAAAAGGCCCTTACATCCCTCACAGGTGTTTGGGCCA	4344	Db	5363	ATACGTACATGGTACCCAAATAATGCTAGCCACTGTGTATTGACTGCCCCCACTCTGCAC	5422
QY	312	-----	312	QY	487	-----	487
Db	4345	GCTCTGACCCCTGGTCTCCACACCCACAGGCAGAGCCCTGCGAGACCTTCT	4404	Db	5423	CCCAAGTTCCTGAGCCTCCCTTCACTCCACTTTGACACGGCCCTCCCTTGTGACCTGA	5482
QY	321	euLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAspI	341	QY	488	-----	488
Db	4405	TGCTGATGAGTCCCGCCAGCTGTACGAGCATTTCCGGGTGACTATCAGACATGACA	4464	Db	5483	GGGCAAGTCCCACTCTGCTCGGAGGAGCGCATGGCGAGTGTCTGACGCCACGGGC	5542
QY	341	leGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArg	358	QY	500	ThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuVal	519
Db	4465	TTGGCTGGAGTGAGGAGCGAGCCAGCACAGTGCTACAGCCTGGCAGCGCGCTTGTGTC	4524	Db	5543	ACCAGTGTGCTACTCACATCCATCAACAACATGGCCGCTCTCTCATGTGTCCTCGTT	5602
QY	358	-----	358	QY	520	ProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPhe	539
Db	4525	AGTCTGGTATGGAACAGGACAAGGGGGTCCCTGAGGCCATTCCTCTCTGCCCCCT	4584	Db	5603	CCCATCCCTCGCTGCGAGCCTTCTCCCTACAGCGCGCCATAGTGTGTGGCTGACCTTT	5662
QY	359	-----	359	QY	540	ValAlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCys	559
Db	4585	CCPATCACCCCTGTTTCTC-CAGCTGGCCAGAGGCCCTCGCTGAGAACGCTTCCGAGC	4643	Db	5663	GTAGCGGTGATGCTTCTTCCAGCCATCCTCAGCCTGGACTACGGCGGCCACTGTC	5722
QY	374	-----	374	QY	560	GlnArgLeuAspValLeuCysCysPheSer	569
Db	4644	AGATCCATGCTTCTCTCCACCACTGGATGACATCTGTCATGCTTCTGAAAGTCA	4703	Db	5723	CAGCGCTTGAATGCTCTGCTGCTTCTC-CAGGTACTGCTGCGCCCCAGCCCCCTTCT	5781
QY	394	erAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu	406	QY	569	-----	569
Db	4704	GTGCTGCCGTGTGGTGGAGGCTAICTGCTCATGGT-GGGTCTTGCACTGGCACCTTG	4762	Db	5782	CCGTCACCCACGCCAGCCTGTCCCTCACAGCATTTTCAAGGCACAGACCTGTCAATCCA	5841
QY	406	-----	406	QY	570	-----	570
Db	4763	CCCCCACCCCTCCAAACAGTGCCACCCCTGGAGCCCTGAGACTGCCCTTTCCCCC	4822	Db	5842	CTCTACCTCTTCCAGTCCCTGCTCTGTCTCAGTGATTCAGATCTCTGCCAGGAGCTG	5901
QY	407	-----	407	QY	585	GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr	604
Db	4823	CACAGCTGGGCTATGCTGTGTACCATGTGCGGGTGGGACTGCGCCAGTCCAGGGTT	4882	Db	5902	GGGACGGGACACTACAGTGGCATTGCCCACTCTCCTCAGTCCAGTTCAGGCTTTACC	5961
QY	424	erValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuLeuC	444	QY	605	HisCysGluAlaSerSerGlnHisValValThrIleLeuProGlnAlaHisLeuVal	624
Db	4883	CCGTGGGCTTCCGGGGTACTGCTGTGGCCCTGGCGGTGGCTCAGGCTTGGGCTCT	4942	Db	5962	CACGTGAAGCCAGCAGCAGCATGTGGTCACCATCTCTGCCCAAGCCCACTGGTG	6021
QY	444	ysAlaLeuLeuGlyIleThrPheAsnAlaThrThr	456	QY	625	ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644
Db	4943	GTGCCCTGCTCGGCATCACCTTCAATGTGCCACTACCCAGGTACGCCAGGACTGCAGGG	5002	Db	6022	CCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTTCAGCCCTGGAGGGTCCACACGGAC	6081
QY	456	-----	456	QY	645	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664
Db	5003	CAGACTCAGTGCCAGTCAACAGGCTTACGGGTCTCAGTGCCTGCTCTCTGCCCCCTC	5062	Db	6082	CTTCTAGGCAGGAGGAGAGACAGGCAAGGACGCTGCAAGTCCCTGCTGCTGCTGCC	6141
QY	457	GlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHis	476	QY	665	ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis	684
Db		-----		Db	6142	CGTGGAAATCTGCCCAATTTGCCCGCGCTATCAGTTTGGCCCCGTTGCTGCTCCAGTCAAT	6201

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	6272	100.0	1203	2	AA089375	Aa089375 homo sapi
2	6272	100.0	1211	2	A6UX14	Q6ux14 homo sapien
3	6272	100.0	1211	2	AA088919	Aa088919 homo sapi
4	6258	99.8	1203	1	PTC2_HUMAN	Q9y6c5 homo sapien
5	5599	89.3	1203	1	PTC2_MOUSE	Q35595 mus musculu
6	5599	89.3	1182	2	CAC88120	Cac88120 mus muscu
7	4119	65.7	1413	2	Q9DEF3	Q9def3 xenopus lae
8	4106	65.5	1422	2	A61RA5	Q61ra5 xenopus lae
9	4106	65.5	1422	2	AAH70395	AaH70395 xenopus l
10	4042.5	64.5	1220	1	PTC1_BRARE	Q98664 brachydanio
11	3348	53.4	1447	1	PTC1_HUMAN	Q13635 homo sapien
12	3344	53.3	913	2	Q90XB9	Q90xb9 gallus gall
13	3340	53.3	1442	1	PTC1_CHICK	Q90693 gallus gall
14	3339.5	53.2	1434	2	Q6UV90	Q6uy90 rattus norv
15	3339.5	53.2	1434	2	AA067738	Aa067738 rattus no
16	3337	53.2	1434	1	PTC1_MOUSE	Q6115 mus musculu
17	3308	52.7	1239	2	Q9DEF4	Q9def4 xenopus lae
18	3308	52.7	1418	2	Q98SW6	Q98sw6 xenopus lae
19	3253	51.9	1243	2	Q9W6T6	Q9w6t6 brachydanio
20	2242	35.7	1318	2	Q9XPY5	Q9xpy5 junonia coe
21	2025.5	32.3	1157	2	Q702Y4	Q702y4 anopheles g
22	1992	31.8	1286	1	PATC_BROME	P18502 dirosophila
23	1812	28.9	651	2	Q6TKFP9	Q6tkp9 homo sapien
24	1812	28.9	651	2	AA821239	AaR21239 homo sapi
25	1776.5	28.3	608	2	Q922A1	Q922a1 rattus norv
26	1708.5	27.2	1405	1	PTC1_CAEEL	Q99614 caenorhabdi
27	1625	25.9	1388	2	Q9NAA1	Q9naa1 caenorhabdi
28	1623.5	25.9	1391	2	Q9SY30	Q9sy30 caenorhabdi
29	992	15.8	714	2	Q09540	Q09540 caenorhabdi
30	984	15.7	255	1	PTC2_CYPN	A42334 cynops pyrr
31	866.5	13.8	287	2	Q9DDZ0	Q9ddz0 xenopus lae

Db 241 AQVQAYVGRPCCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGSHKFMHQBELLG 300
QY 301 GWARDPQGLLRAELAQSTFLMSPPQLYEHFRGDYQTHDIGWSEBQASTVLQAWORRV 360
Db 301 GWARDPQGLLRAELAQSTFLMSPPQLYEHFRGDYQTHDIGWSEBQASTVLQAWORRV 360
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Db 361 QLAQALPENASQOIHAFSSTLDDILHAFSEVSARVVGYYLLMLAYACVTMLRWDCAQ 420
QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATTQVLFPFALGIGVDVFLAHAFTE 480
Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATTQVLFPFALGIGVDVFLAHAFTE 480
QY 481 ALPGTLPQRMGECLQRTGTSVVLTSINNMAFLMAALVPIPALRAFSLQAAIVVGCTTV 540
Db 481 ALPGTLPQRMGECLQRTGTSVVLTSINNMAFLMAALVPIPALRAFSLQAAIVVGCTTV 540
QY 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDTVPVGIHAHTATV 600
Db 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDTVPVGIHAHTATV 600
QY 601 QAFTHCEASSQHVVTILPQAHLVPPSPDLGSELPSPGSTRDLGQBEETRQKAACKS 660
Db 601 QAFTHCEASSQHVVTILPQAHLVPPSPDLGSELPSPGSTRDLGQBEETRQKAACKS 660
QY 661 LPCARNLAFHARYQAPILLOSHAKAIVLVIFGALLGLSLYCATIVQDGLATDVVPRG 720
Db 661 LPCARNLAFHARYQAPILLOSHAKAIVLVIFGALLGLSLYCATIVQDGLATDVVPRG 720
QY 721 TREHAFSLAQRLYFSLYEVALVTQGGFDVAHSORALFDLHORFSSLKAVLPPPAQAPRT 780
Db 721 TREHAFSLAQRLYFSLYEVALVTQGGFDVAHSORALFDLHORFSSLKAVLPPPAQAPRT 780
QY 781 WLHYRNWLQGIQAAPDQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQBPLDFSQT 840
Db 781 WLHYRNWLQGIQAAPDQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQBPLDFSQT 840
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Db 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWHLHDKYDTTGENLRIP 900
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Db 901 PAQPLEFAFPFLLRGLQKTADVEAIEGARAACAGAGVHAYPSGSPFLFWEQYGL 960
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Db 961 RRCFLAVCILLVCTFLVCAILLNPWTAGLIVLVLAMMTVELFGIMFLGIKLSAIPVV 1020
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Db 1081 FDFIVRYFAALTVLTLGLLHGLVLLPVLLSLTILGPPPEVIQMYKESPELSPAPQGGG 1140
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Db 1141 LRWGASSSLPQSFARVTTSMVAIHPPPLPGAYIHPADPEPWPSPAAATSSGNLSRGP 1200
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Db 1201 ATG 1203

RESULT 2

Q6UX14 PRELIMINARY; PRT; 1211 AA.
ID Q6UX14
AC Q6UX14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Patched 2.
GN ORFNames=UNQ560;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klinkowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358555; AAQ88919.1; -.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD_5TM.
DR Pfam; PF02460; Patched; 1.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
SQ SEQUENCE 1211 AA; 131568 MW; 303D4FC55D39FB77 CRC64;

Query Match 100.0%; Score 6272; DB 2; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRSPRLPSPSYTPPARTAAPQILAGSLKAPLMRAYFQGLLFLSGGIGRHCCKVLF 60
Db 1 MTRSPRLPSPSYTPPARTAAPQILAGSLKAPLMRAYFQGLLFLSGGIGRHCCKVLF 60
QY 61 LGLAFGALALGLRMAIETNLEQLWVEVGSRSVQELHYTKELGEEAAYTSQMLIQAR 120
Db 61 LGLAFGALALGLRMAIETNLEQLWVEVGSRSVQELHYTKELGEEAAYTSQMLIQAR 120
QY 121 QGENILTPREALGLHQAALTASKQVSLYKSWDLNKKCYKSGVPLIENGMIEMLEKL 180
Db 121 QGENILTPREALGLHQAALTASKQVSLYKSWDLNKKCYKSGVPLIENGMIEMLEKL 180
QY 181 FPCVILTLDCEWEGAKLOGGSAYLPGRPDIOWTNLDPEQLLEELGPFASLEGFRELDDK 240
Db 181 FPCVILTLDCEWEGAKLOGGSAYLPGRPDIOWTNLDPEQLLEELGPFASLEGFRELDDK 240
QY 241 AQVQAYVGRPCCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGSHKFMHQBELLG 300
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Db 481 ALPGTLPQRMGECLQRTGTSVVLTSINNMAFLMAALVPIPALRAFSLQAAIVVGCTTV 540
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Db 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVLIQLPQELGDTVPVGHIAHTATV 600
QY 601 QAFTHCEASSQHVVTILPPQAHVLPVPPDPLGSELSPGSGTRDLGQEBETRQKAACKS 660
Db 601 QAFTHCEASSQHVVTILPPQAHVLPVPPDPLGSELSPGSGTRDLGQEBETRQKAACKS 660
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Db 661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVLFAGLLGLSLYGATLVODGLATDVVPRG 720
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Db 721 TKEHAFSLAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRFPSSKAVLPPPPATQAPT 780
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Db 841 TRKLVREGLIPELFFMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQFPFLRLGLQKTADFEVAIEGARAAAEAGAGVHAYPSGSPFLFWEQYVGL 960
Db 901 PAQPLEFAQFPFLRLGLQKTADFEVAIEGARAAAEAGAGVHAYPSGSPFLFWEQYVGL 960
QY 961 RRCFLAVCILLVCTFLVCALLLNPTAGLIVLVLMNTVELFGIMFGIKLSAIPVV 1020
Db 961 RRCFLAVCILLVCTFLVCALLLNPTAGLIVLVLMNTVELFGIMFGIKLSAIPVV 1020
QY 1021 ILVASGIGVEFTVHVVALGFLTTQGSNRNRAHALESHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASGIGVEFTVHVVALGFLTTQGSNRNRAHALESHTFAPVTDGAISTLLGLMLAGSH 1080
QY 1081 FDFIVRYFFAALTTLTLLGLHGLVLLPVLLSILGPPPEVIOMYKESPELSPAPQGGG 1140
Db 1081 FDFIVRYFFAALTTLTLLGLHGLVLLPVLLSILGPPPEVIOMYKESPELSPAPQGGG 1140
QY 1141 LRWGASSLPQSFAVTTSMVAIHPPPLPGAYIHPADPEPWSPAATSSGNLSRSGPGP 1200
Db 1141 LRWGASSLPQSFAVTTSMVAIHPPPLPGAYIHPADPEPWSPAATSSGNLSRSGPGP 1200
QY 1201 ATG 1203
Db 1201 ATG 1203

RESULT 3
AAQ88919 ID AAQ88919 PRELIMINARY; PRT; 1211 AA.
AC AAQ88919;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE Patched 2.
GN UNQ560.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1) _
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Huang L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;

RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358555; AAQ88919.1; -;
SQ SEQUENCE 1211 AA; 131568 MW; 303D4FC55D39FB77 CRC64;
Query Match 100.0%; Score 6272; DB 2; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTRSPRLRELPSYTPPARTAQAQIILAGSLKAPLMLRAYFOGLLPSLGGCIQHRHCKVLF 60
Db 1 MTRSPRLRELPSYTPPARTAQAQIILAGSLKAPLMLRAYFOGLLPSLGGCIQHRHCKVLF 60
QY 61 LGLLAFGALALGLRMAIIEITNLEQLWVEVGSRSVQELHYTKELGEEAAYTSQMLQTAR 120
Db 61 LGLLAFGALALGLRMAIIEITNLEQLWVEVGSRSVQELHYTKELGEEAAYTSQMLQTAR 120
QY 121 QEGENILTPALGLHLQAALTASKVQVSLYKGSWDLNKI CYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENILTPALGLHLQAALTASKVQVSLYKGSWDLNKI CYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDLCFWEKAKLOGGSAYLPRPDIQWNTNLDPPQLLEELGFPFASLEGFRELDDK 240
Db 181 FPCVILTPDLCFWEKAKLOGGSAYLPRPDIQWNTNLDPPQLLEELGFPFASLEGFRELDDK 240
QY 241 AQVGQAYVGRPCILHPDDLHCPPSAPNHHGRQAPNVAHELSSGGCHGFSHKFMHWEQELLG 300
Db 241 AQVGQAYVGRPCILHPDDLHCPPSAPNHHGRQAPNVAHELSSGGCHGFSHKFMHWEQELLG 300
QY 301 GWARDPQGBELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIQWSEEQASTVLQAWORRFV 360
Db 301 GWARDPQGBELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIQWSEEQASTVLQAWORRFV 360
QY 361 QLAQALPENASQOIHAFSSTTLDLILHAFSVAARVGVGVLMLLAYACVMTLRLWDCAQ 420
Db 361 QLAQALPENASQOIHAFSSTTLDLILHAFSVAARVGVGVLMLLAYACVMTLRLWDCAQ 420
QY 421 SQSGVGLAGVLVLAVALASGLGICALLGITFNAATTQVLPFLALGIGVDDVLLAHAFTE 480
Db 421 SQSGVGLAGVLVLAVALASGLGICALLGITFNAATTQVLPFLALGIGVDDVLLAHAFTE 480
QY 481 ALPGTPLQERMGECLQRTGTSVLTSSINMAAFLMAALVPIIPALRAFSLQAALVVGCTFV 540
Db 481 ALPGTPLQERMGECLQRTGTSVLTSSINMAAFLMAALVPIIPALRAFSLQAALVVGCTFV 540
QY 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVLIQLPQELGDTVPVGHIAHTATV 600
Db 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVLIQLPQELGDTVPVGHIAHTATV 600
QY 601 QAFTHCEASSQHVVTILPPQAHVLPVPPDPLGSELSPGSGTRDLGQEBETRQKAACKS 660
Db 601 QAFTHCEASSQHVVTILPPQAHVLPVPPDPLGSELSPGSGTRDLGQEBETRQKAACKS 660
QY 661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVLFAGLLGLSLYGATLVODGLATDVVPRG 720
Db 661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVLFAGLLGLSLYGATLVODGLATDVVPRG 720
QY 721 TKEHAFSLAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRFPSSKAVLPPPPATQAPT 780
Db 721 TKEHAFSLAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRFPSSKAVLPPPPATQAPT 780
QY 781 WLHYRNWLOGIOQAADFQDQWASGRITRHSYRNGSEGDALAYKLLIQTGDAQEPDLSQLT 840
Db 781 WLHYRNWLOGIOQAADFQDQWASGRITRHSYRNGSEGDALAYKLLIQTGDAQEPDLSQLT 840
QY 841 TRKLVREGLIPELFFMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVREGLIPELFFMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQFPFLRLGLQKTADFEVAIEGARAAAEAGAGVHAYPSGSPFLFWEQYVGL 960

FT	VARSPIC	1143	1203	WGASSLPQSFAVTTMTVAHPPLPGAYIHAPDEPPW SPATSSGNLSRGPGATG -> PEEI (in isoform 2)..	
FT				/FTid=vsp_004542.	
FT	VARIANT	346	346	E -> Q.	
FT				/FTid=var_018935.	
FT	VARIANT	493	493	E -> K.	
FT				/FTid=var_018936.	
FT	VARIANT	622	622	H -> Y.	
FT				/FTid=var_018937.	
FT	VARIANT	988	988	T -> M.	
FT				/FTid=var_018938.	
FT	VARIANT	1019	1019	V -> M.	
FT				/FTid=var_018939.	
FT	VARIANT	1121	1121	I -> M.	
FT				/FTid=var_018940.	
FT	CONFLICT	2	2	T -> N (in Ref. 2).	
FT	CONFLICT	120	120	R -> L (in Ref. 2).	
FT	CONFLICT	175	175	R -> W (in Ref. 2).	
FT	CONFLICT	753	753	O -> R (in Ref. 1).	
FT	CONFLICT	787	787	N -> S (in Ref. 2).	
FT	CONFLICT	833	833	P -> L (in Ref. 3).	
FT	CONFLICT	837	837	S -> G (in Ref. 2).	
FT	CONFLICT	846	846	D -> E (in Ref. 2).	
FT	CONFLICT	897	897	L -> F (in Ref. 3).	
FT	SEQUENCE	1203 AA;	130543 MW;	4FAB06999782C031 CRC64;	
QY	Query Match			99.8%; Score 6258; DB 1; Length 1203;	
Db	Best Local Similarity			99.9%; Pred. No. 0;	
Db	Matches 1202; Conservative			0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	MTRSPRLRLPSYTPPARTAAPQIILAGSLKAPLMRAYFOGLFSLGCGIORHCKVLF	60		
Db	1	MTRSPRLRLPSYTPPARTAAPQIILAGSLKAPLMRAYFOGLFSLGCGIORHCKVLF	60		
QY	61	LGLLAFGALGLRMAIIEITNLEQLWVEVGSRSOELHYTKEKLGEEAAYTSQMLIQIAR	120		
Db	61	LGLLAFGALGLRMAIIEITNLEQLWVEVGSRSOELHYTKEKLGEEAAYTSQMLIQIAR	120		
QY	121	QGENILTPALGLHLQALATSKVQVSLYKSWDLNKKCYKSGVPLIENGMIEMIEKL	180		
Db	121	QGENILTPALGLHLQALATSKVQVSLYKSWDLNKKCYKSGVPLIENGMIEMIEKL	180		
QY	181	FPVILTPDLCWEKAGKGGAYLPGRPDIQWNLDPQILLEELGPFASLEGFRELDDK	240		
Db	181	FPVILTPDLCWEKAGKGGAYLPGRPDIQWNLDPQILLEELGPFASLEGFRELDDK	240		
QY	241	AQVGQAYVGRPCLHPDDLCPSPAPNHHSRQAPNVAHELSGGCHGFSHKFMHQBELLLG	300		
Db	241	AQVGQAYVGRPCLHPDDLCPSPAPNHHSRQAPNVAHELSGGCHGFSHKFMHQBELLLG	300		
QY	301	GMARDPOGELLRAEALQSTFLMSRQLYVEHFRGDIQWNLDPQILLEELGPFASLEGFRELDDK	360		
Db	301	GMARDPOGELLRAEALQSTFLMSRQLYVEHFRGDIQWNLDPQILLEELGPFASLEGFRELDDK	360		
QY	361	QLAQALPENASQQLHAFSSITLDDILHAFSVSAARVVGYYLLMAYACVTMLRDCAQ	420		
Db	361	QLAQALPENASQQLHAFSSITLDDILHAFSVSAARVVGYYLLMAYACVTMLRDCAQ	420		
QY	421	SGSVGLAGVLLVALAVASGLCALGTLTFNAATQVLPFLALGIVGDDVFLLAHAFTE	480		
Db	421	SGSVGLAGVLLVALAVASGLCALGTLTFNAATQVLPFLALGIVGDDVFLLAHAFTE	480		
QY	481	ALPGTFLQRMGECLQRTGTSVLTSSINMAFLMAALVPIPALRAFSLQAAIVVGCTFV	540		
Db	481	ALPGTFLQRMGECLQRTGTSVLTSSINMAFLMAALVPIPALRAFSLQAAIVVGCTFV	540		
QY	541	AVMLVFPALSLDLRRHRCORLDVLCFSSPCSAQVILPQELGDTVPVGIHLTATV	600		
Db	541	AVMLVFPALSLDLRRHRCORLDVLCFSSPCSAQVILPQELGDTVPVGIHLTATV	600		
QY	601	QAFTHCEASSQHWVTILPQAHVLPVPPSDPLGSELFPQGSRTDLLGQEEETROKAAACKS	660		

Db	601	QAFTHCEASSQHWVTILPQAHVLPVPPSDPLGSELFPQGSRTDLLGQEEETROKAAACKS	660		
QY	661	LPCARWNLAHFARYQFAPLLQSHAKAIVLVLFALLGLSLYGATLVQDGLALTDVVPRG	720		
Db	661	LPCARWNLAHFARYQFAPLLQSHAKAIVLVLFALLGLSLYGATLVQDGLALTDVVPRG	720		
QY	721	TRKHAFLSAQLRYFSLYEVALVTQGGFDYAHQSQRALFDLHQRSSSKAVLPPPAQAPRT	780		
Db	721	TRKHAFLSAQLRYFSLYEVALVTQGGFDYAHQSQRALFDLHQRSSSKAVLPPPAQAPRT	780		
QY	781	WLHYRNWLQGIQAAPDQDQWASGRITRHSYRNGSEDCALAYKLLIOTGDAQEPDLSOLT	840		
Db	781	WLHYRNWLQGIQAAPDQDQWASGRITRHSYRNGSEDCALAYKLLIOTGDAQEPDLSOLT	840		
QY	841	TRKLVDRGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDITTGENLRIP	900		
Db	841	TRKLVDRGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDITTGENLRIP	900		
QY	901	PAQPLEFAQFPFLRLGLOKTADFVEAIEGARAACACAGQAGVHAYPSGSPFLFWEOYLGL	960		
Db	901	PAQPLEFAQFPFLRLGLOKTADFVEAIEGARAACACAGQAGVHAYPSGSPFLFWEOYLGL	960		
QY	961	RRCFLLAVCILLVCTFLVCALLLNPNWPTAGLIVLVLMMTVELFGTMGFLGKLSAIPVV	1020		
Db	961	RRCFLLAVCILLVCTFLVCALLLNPNWPTAGLIVLVLMMTVELFGTMGFLGKLSAIPVV	1020		
QY	1021	ILVASVIGVETVHVVALGFLTQGSRNLRRAHALEHTFAPVTDGAISTLLGLMLAGSH	1080		
Db	1021	ILVASVIGVETVHVVALGFLTQGSRNLRRAHALEHTFAPVTDGAISTLLGLMLAGSH	1080		
QY	1081	FDIVRYVRYFAALTVLTLGLLHGLVLLPVLSILGPPPEVIOMYKESPEILSPAPQGGG	1140		
Db	1081	FDIVRYVRYFAALTVLTLGLLHGLVLLPVLSILGPPPEVIOMYKESPEILSPAPQGGG	1140		
QY	1141	LRWGASSLPQSFAVTTMTVAIHPPPLPGAYIHAPDEPPWSPAATSSGNLSRGPGP	1200		
Db	1141	LRWGASSLPQSFAVTTMTVAIHPPPLPGAYIHAPDEPPWSPAATSSGNLSRGPGP	1200		
QY	1201	ATG 1203			
Db	1201	ATG 1203			

RESULT 5

PTC2 MOUSE

ID	PTC2 MOUSE	STANDARD;	PRT; 1182 AA.
AC	O35595;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Patched protein homolog 2 (PTC2).		
GN	Name=Ptc2;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Embryo;		
RX	MEDLINE=98122566; PubMed=9462734;		
RA	Motoyana J., Takabatake T., Takeshima K., Hui C.-C.;		
RT	"Ptc2, a second mouse patched gene is co-expressed with Sonic		
RT	hedgehog.";		
RL	Nat. Genet. 18:104-106(1998).		
RN	[2]		
RP	SEQUENCE OF 196-446 FROM N.A.		
RC	STRAIN=BALE/c; TISSUE=Neuroretina;		
RX	MEDLINE=97379366; PubMed=9237688;		
RA	Takabatake T., Ogawa M., Takahashi T.C., Mizuno M., Okamoto M.,		
RT	Takeshima K.;		
RT	"Hedgehog and patched gene expression in adult ocular tissues.";		
RL	FEBS Lett. 410:485-489(1997).		
CC	!- FUNCTION: May have a role in epidermal development. May act as a		

CC receptor for Sonic hedgehog (SHH).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in epithelial cells of the
 CC developing hair, tooth and whisker.
 CC -!- DEVELOPMENTAL STAGE: Detected in 8.5 to 17.5 dpc embryos.
 CC -!- SIMILARITY: Belongs to the patched family.
 CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
 CC
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB010833; BAA24691.1; -.
 CC FIR; T13952; T13952.
 CC MGD; MG1:1095405; Ptc2.
 CC InterPro; IPR003392; Patched.
 CC InterPro; IPR004766; Patchedtm_recept.
 CC InterPro; IPR000731; SSD_5TM.
 CC Pfam; PF02460; Patched; 1.
 CC TIGRFAMs; TIGR00918; 2A060602; 1.
 CC PROSITE; PS00156; SSD; 1.
 CC Glycoprotein; Receptor; Transmembrane.
 KW DOMAIN 1 57 Cytoplasmic (Potential).
 FT TRANSMEM 58 78 Potential.
 FT DOMAIN 79 394 Extracellular (Potential).
 FT TRANSMEM 395 414 Potential.
 FT DOMAIN 415 428 Cytoplasmic (Potential).
 FT TRANSMEM 429 449 Potential.
 FT DOMAIN 450 457 Extracellular (Potential).
 FT TRANSMEM 458 478 Potential.
 FT DOMAIN 479 501 Cytoplasmic (Potential).
 FT TRANSMEM 502 521 Potential.
 FT DOMAIN 523 531 Extracellular (Potential).
 FT TRANSMEM 532 552 Potential.
 FT DOMAIN 553 686 Cytoplasmic (Potential).
 FT TRANSMEM 687 707 Potential.
 FT DOMAIN 708 963 Extracellular (Potential).
 FT TRANSMEM 964 984 Potential.
 FT DOMAIN 985 991 Cytoplasmic (Potential).
 FT TRANSMEM 992 1012 Potential.
 FT DOMAIN 1013 1033 Extracellular (Potential).
 FT TRANSMEM 1034 1034 Potential.
 FT DOMAIN 1035 1064 Cytoplasmic (Potential).
 FT TRANSMEM 1065 1085 Potential.
 FT DOMAIN 1086 1086 Extracellular (Potential).
 FT TRANSMEM 1087 1107 Potential.
 FT DOMAIN 1108 1182 Cytoplasmic (Potential).
 FT TRANSMEM 1182 1182 SSD.
 FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 812 812 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 1182 AA; 128585 MW; 715233D912C352F2 CRC64;
 Query Match 89.3%; Score 5599; DB 1; Length 1182;
 Best Local Similarity 90.9%; Pred. No. 0;
 Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;
 QY 1 MTRSPRLPLPSYTPPARTAQAQILAGSLKAPLMLRAYFQGLLSLGGCIGRHCCKVLF 60
 Db 1 MYRPLSLGLPLPSYTPPARTASSAPHILLAGSLQAPLMLRAYFQGLLSLGGCIGRHCCKVLF 60
 QY 61 LGLLAFGALALGLRMAIETNLEQLWVEVSGSRVSRVQELHYTKEKLGEEAAYTSOMLIQTAR 120
 Db 61 LGLVAFGALALGLRVAIVETDLEQLWVEVSGSRVSRVQELHYTKEKLGEEAAYTSOMLIQTAR 120
 QY 121 QEGENTLTPEALGLHQAALTASKQVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
 Db 121 QEGGNVLTPEALDLHQAALTASKQVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
 QY 181 FPCVILTPDCEWEGAKLQGSAYLFGRPDIQWNTLDPQELLEELGFPFASLEGFRELDDK 240

Db 181 FPCVILTPDCEWEGAKLQGSAYLFGRPDIQWNTLDPQELLEELGFPFASLEGFRELDDK 240
 QY 241 AQVQAYVGRPCLDHPDDLHCPSPANHHSRQAPNVAHELSCGCHFSKFMHWQEBLLG 300
 Db 241 AQVQAYVGRPCLDHPDDHCPSPANRHSRQAPNVAQELSGCHFSKFMHWQEBLLG 300
 QY 301 GMRPPOGELLRAELAQSTFLLMSPROLYHEHFRGYQTHDLCWSEEQASTVLQAMORRV 360
 Db 301 GTARDLQGLLRAELAQSTFLLMSPROLYHEHFRGYQTHDLCWSEEQASTVLQAMORRV 360
 QY 361 QLAQALPENASQOIHAFSTTDLDDLHAFSEVSAARVVGGLYLLMLAYACVTLMLRWDCAQ 420
 Db 361 QLAQALPANASQOIHAFSTTDLDDLILRAFSEVSTRVVGGLYLLMLAYACVTLMLRWDCAQ 420
 QY 421 SQGSVGLAGVLIVAVASGLGLCALGLITFNAAQTQVLPFLALGIGVDVFLAHAFTE 480
 Db 421 SQGAVGLAGVLIVAVASGLGLCALGLITFNAAQTQVLPFLALGIGVDVFLAHAFTE 480
 QY 481 ALPGTPLQERMGECLQRTGTSVLTSTNNMAFLMAALVPIPALRAFSLQAAIVVGCFTV 540
 Db 481 APPDTPLPERMGECLRSTGTSVALTSVNNWVAFMAALVPIPALRAFSLQAAIVVGCFTV 540
 QY 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQILPOELGDTGTVPGTAHLTATV 600
 Db 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQMLPOELGDRVAVPGIAHLTATV 600
 QY 601 QAFTHCEASSQHVVTILPPQAHLLVPPSPDLGSELPSGSGSTRDLLGQBEETROKAACKS 660
 Db 601 QAFTHCEASSQHVVTILPPQAHLLSPASDLGSELYSPGSGSTRDLLSQEGTGPQACRP 660
 QY 661 LPCAENWLAHFARYOFAPILLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTVDVVRG 720
 Db 661 LICAHTWLAHFARYOFAPILLQTRAKALVLLFPGALLGLSLYGATLVQDGLALTVDVVRG 720
 QY 721 TKEHAFSLAQLRYFSLYEVALVTQGFQDYAHQORALFDLHQRFSSIKAYLPPFPATQAPT 780
 Db 721 TXEHAFSLAQLRYFSLYEVALVTQGFQDYAHQORALFDLHQRFSSIKAYLPPFPATQAPT 780
 QY 781 WLHYRNWMLQIOAAPDQWASGRITRHSYRNGSEDEGALAYKLLIQTGDAQEPDLSOLT 840
 Db 781 WLHYRWSWMLQIOAAFDQWASGRITCHSYRNGSEDEGALAYKLLIQTGNAQEPDLSOLT 840
 QY 841 TRKLVDRGLIPPELFYMGSLTVWVSSDPLGLAASQANFYPPPEMLHDKYDTTGENLRIP 900
 Db 841 TRKLVDRGLIPPELFYMGSLTVWVSSDPLGLAASQANFYPPPEMLHDKYDTTGENLRIP 900
 QY 901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
 Db 901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
 QY 961 RRCFLAVCILVCTFLVCALLLNPNWTAGLIVLVMAMTVLFGIMGLGKLSAIPV 1020
 Db 961 RRCFLAVCILVCTFLVCALLLNPNWTAGLIVLVMAMTVLFGIMGLGKLSAIPV 1020
 QY 1021 ILVASGIGVEFTVHVALGFLTTCQSRNLRRAHALEHTFAPVTDGTAISTLLGLMLAGSH 1080
 Db 1021 ILVASGIGVEFTVHVALGFLTSHGSRNLRRAHALEHTFAPVTDGTAISTLLGLMLAGSH 1080
 QY 1081 FDFIVRYFFAALTTLTLLGLLHGLVLLPVLLSLGPPPEVIOMYKESPEILSPAPQGG 1140
 Db 1081 FDFIIRYFFVLTTLTLLGLLHGLLVPVLLSLGPPPVQVQVYKESPTLNSAAPQGG 1140
 QY 1141 LRWGASSUSLPQSFARVTTSMVAIHPPPLPGAYIHPADEP 1181
 Db 1141 LRWDPRPTLPQSFARVTTSMVAIHPPPLPGAYIHPASEP 1181
 RESULT 6
 CAC88120
 ID CAC88120 PRELIMINARY; PRT; 1182 AA.
 AC CAC88120;
 DT 02-MAR-2004 (TREMBLrel. 27, Created)

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02-MAR-2004 (TREMBlrel. 27, Last sequence update)
02-MAR-2004 (TREMBlrel. 27, Last annotation update)
Patched 2 protein.
PTCH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SvJ; TISSUE=Liver;
RA Froehlich L., Zhanquin L., Beier D.R., Lanske B.;
RT "Genomic structure and refined chromosomal localization of the mouse
RT ptch2 gene.";
RL Cytogenet. Genome Res. 97:106-110(2002).
DR EMBL; AJ133482; CAC88120.1; -.
DR EMBL; AJ133483; CAC88120.1; JOINED.
DR EMBL; AJ133484; CAC88120.1; JOINED.
DR EMBL; AJ133485; CAC88120.1; JOINED.
SQ SEQUENCE 1182 AA; 128585 MW; 7152333D912C352F2 CRC64;

Query Match      89.3%; Score 5599; DB 2; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

QY 1 MTRSPPLRELPSYTPPTAPTRAPQILAGSLKAPLMRLAYFQGLIFSLGCGIQHRCCKVLF 60
Db 1 MYRPLSLGELPSYTPPTAPTRAPQILAGSLKAPLMRLAYFQGLIFSLGCGIQHRCCKVLF 60
QY 61 LGLAFGALALGLRMAIETNLEQLWVEVGSVSOELHYTKELGEEAAYTSQMLIQTAH 120
Db 61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSVSOELHYTKELGEEAAYTSQMLIQTAH 120
QY 121 QGGENILTPALGLHLQAALTAASKVQVSLYKSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
Db 121 QEGGNVLTPEALDLHLQAALTAASKVQVSLYKSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPLDCFEWEGAKQGGSAIYLPGRDIOWTNLDPEQLLEELGPPASLGFFRELDK 240
Db 181 FPCVILTPLDCFEWEGAKQGGSAIYLPGRDIOWTNLDPEQLLEELGPPASLGFFRELDK 240
QY 241 AQVGAYVGRPCLDHDLHCPSPAPNHHSRQAPNVAHLSGGCHGFSHKFMHWQELLIG 300
Db 241 AQVGAYVGRPCLDHDLHCPSPAPNHHSRQAPNVAHLSGGCHGFSHKFMHWQELLIG 300
QY 301 GMRAPQBELLRALQSTFLLMSRQLYEHPRGYQTHDIGWSEBQASTVLQAWQRFRV 360
Db 301 GTARDLQGLLRALQSTFLLMSRQLYEHPRGYQTHDIGWSEBQASTVLQAWQRFRV 360
QY 361 QLAQALPENASQOITHAFSTTLDLILHAFSEVSAARVVGGLLMLAYACVTMLRWDCAQ 420
Db 361 QLAQALPANASQOITHAFSTTLDLILHAFSEVSAARVVGGLLMLAYACVTMLRWDCAQ 420
QY 421 SQGSVGLAGLVALLAVASGLGLCALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFTE 480
Db 421 SQGAVGLAGLVALLAVASGLGLCALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFTE 480
QY 481 ALPGTPLQRMGECIQRGTSTVLTSTNNMAFLMAALVPIPALRAFSLQAAIIVGCTTV 540
Db 481 APPDTPLQRMGECIQRGTSTVLTSTNNMAFLMAALVPIPALRAFSLQAAIIVGCTTV 540
QY 541 AVMLVFPAILSLDLRRRHCRDLVLCFSSPCSAQVQIQLPQELGDTVPVGHIAHTATV 600
Db 541 AVMLVFPAILSLDLRRRHCRDLVLCFSSPCSAQVQIQLPQELGDTVPVGHIAHTATV 600
QY 601 QAFTHCEASSQHVVTILPPOAHLVPPPPDPLGSELFPSSGSTRDLIGQEEETROKAAACKS 660
Db 601 QAFTHCEASSQHVVTILPPOAHLVPPPPDPLGSELFPSSGSTRDLIGQEEETROKAAACKS 660
QY 661 LPCARNLHAHFARYQFAPLLQLQSHAKAIVLVLFGLALLGLSLYGATLVQDGLALTVDVPRG 720
Db 661 LILCAHWTLAHFARYQFAPLLQLQSHAKAIVLVLFGLALLGLSLYGATLVQDGLALTVDVPRG 720

121 TKEHAFSLAQIRYFSLYEVALVTQGGFDYAHQSORALFDLHORFSSLKAVLPPATQAPRT 780
721 TKEHAFSLAQIRYFSLYEVALVTQGGFDYAHQSORALFDLHORFSSLKAVLPPATQAPRT 780
781 WLHYRNMLQGIQAAAFDQDQWASGRITRHSYRNGSEGDALAYKLLIQTGDAQBPLDFSOLT 840
781 WLHYRSMVQGIQAAAFDQDQWASGRITRHSYRNGSEGDALAYKLLIQTGDAQBPLDFSOLT 840
841 TRKLVDRGLIPELFFYMGSLTVWSSDPLGLAASQANFYPPPEWLHDKYDITTTGENLRIP 900
841 TRKLVDRGLIPELFFYMGSLTVWSSDPLGLAASQANFYPPPEWLHDKYDITTTGENLRIP 900
901 PAQPLEFAQFPFLRLGLQKTADPFAIEGARAACAEAGQAGVHAYPSGSPFFLFWEOYLGL 960
901 AAQPLEFAQFPFLRLGLQKTADPFAIEGARAACAEAGQAGVHAYPSGSPFFLFWEOYLGL 960
961 RRCFLAVCILLVCTFVLCALLLPLWPTAGTLVLVLAAMTVLFGIMGLKLSAIPVV 1020
961 RECFLAVCILLVCTFVLCALLLPLWPTAGTLVLVLAAMTVLFGIMGLKLSAIPVV 1020
1021 ILVASVIGVEFTVHVALGFLTQGSRNLRRAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
1021 ILVASIGIGVEFTVHVALGFLTSHGSRNLRRAASALEQTFAPVTDGAVSTLLGLMLAGSN 1080
1081 FDFIVRYFAALTTLGLLGLHVLPLVLSILGPPPEVIOYKESPEILSPAPQGG 1140
1081 FDFIIRYFVFWLTVTLGLLGLHVLPLVLSILGPPPEVIOYKESPEILSPAPQGG 1140
1141 LRWGASSILPQSFAVTTSMVTHIHPPLPGAYIHPADPEP 1181
1141 LEWDPPPTLPQSFAVTTSMVTHIHPPLPGAYIHPADPEP 1181

RESULT 7
Q9DEF3 PRELIMINARY; PRT; 1413 AA.
AC Q9DEF3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Patched-2.
GN Name=Xotch-2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20500895; PubMed=11044611;
RA Takabatake T., Takahashi T.C., Takabatake Y., Yamada K., Ogawa M.,
RA Takashima K.;
RT "Distinct expression of two types of Xenopus Patched genes during
RT early embryogenesis and hindlimb development.";
EL Mech. Dev. 98:99-104(2000).
DR EMBL; AB037688; BAB18575.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008158; F:hedgehog receptor activity; IEA.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR00731; SSD_5TM.
DR Pfam; PF02460; Patched; I.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
SQ SEQUENCE 1413 AA; 157372 MW; 1215D2D7733E7F17 CRC64;

Query Match      65.7%; Score 4119; DB 2; Length 1413;
Best Local Similarity 65.4%; Pred. No. 1e-267;
Matches 789; Conservative 165; Mismatches 213; Indels 39; Gaps 9;

QY 12 PSYTPPTAPQILAGSL---KAPLMRLAYFQGLIFSLGCGIQHRCCKVLFGLGAFGA 68
Db 35 PSYC-HAFAFKQIAKGVAGQKAPLMRLAQFQALLFSLGCGIQHRCCKVLFGLLVEGA 93

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QY 12 PSYTPARTAAPOILAGSL---KAPLWLRAYFOGLLFSLGCGTQORHCGKVFLGLLAFGA 68
Db 35 PSYC-HAFAFKQIAKGVAGKAPLWLRAYFOGLLFSLGCGTQORHCGKVFLGLLAFGA 93
QY 69 LALGLRMAIETNLEOLWEVSRVSOEHLHYTKELGEEAAVTSQMLIQTARQEGENILT 128
Db 94 LAVGLRVASIEITDIERLWEAGSRVSHELRYTKELGEEVTSQMLIQTARKEGNILT 153
QY 129 PEALGHLHQAALTSKQVSLVSKGSDNLNKI CVKSGVPLIENGMIEMIEKLPFPCVILTP 188
Db 154 NEALLHLRAALAASKVQVSMYKSKDNLNKI CVKSGVPIIENGMIEMIEKLPFPCVILTP 213
QY 189 LDCFWEGAMLOGGSAYLPCRPDIOWNLDPOLLELGPFIASLEGPRELLDQAQVOAV 248
Db 214 LDCFWEGSLOGGSAYLPCRADLQWNLDPFKLMEELGQFTSLDGPKEMLDKAEVQGGY 273
QY 249 GRPCLHPDLHCPSPAPNHSRQAPNVAHELSGCHGFSKFMHWQEEELLGGMARDPOG 308
Db 274 ERPCLDPTSDCPESPNNKTKKPKDPIVSTLRGCGYFSGKFMWQKELILGMLKGPDG 333
QY 309 ELRLRALQSTFLMSPROLYHFRGCDYOTHIDIGWSEBOASTVLOQWRFRVQLAQEALP 368
Db 334 ELKSAEALQTMVLLSPGQLYEHFKDDYEHIDINWNEEKAAALLESQWRKFVEQAQOSIP 393
QY 369 ENASQOIHFASSTLDDILHAFSEVSAARVVGYLMLLAYACVTLRWDCASQSGVGLA 428
Db 394 QNSQDIHAFSTTLNDIMKSDSDSAIRVAGGYLLMLLAYACATMLRWDCSKSQGAVGLA 453
QY 429 GVLVALAVASGLGICALGIFTNAATQVLPALGIGVDVDFLLAHAFTEALPCTPLQ 488
Db 454 GVLVALVAVASGLGICALGIFTNAATQVLPALGIGVDVDFLLAHAFTEALPCTPLQ 513
QY 489 ERMGELQRTGTSVLTSTNNWAFIPALRAFSLQAAIVVGTCTFVAVMLVPPA 548
Db 514 ERTGELQRTGTSVLTSTNNWAFIPALRAFSLQAAIVVGTCTFVAVMLVPPA 573
QY 549 ILSLDLRRRCORLDVLCFSPSCSAQVQILPOELGDG-----TVPVGT 594
Db 574 ILSLDLRRRCORLDVLCFSPSCSAQVQILPOELGDG-----TVPVGT 632
QY 595 HLTATVQAFTHCEASSQHVVTILPPOAHLVPPPS-----DPLGSELFPGGSTRDLQ 648
Db 633 QITTVQAFTHCEASSQHVVTILPPOAHLVPPPS-----DPLGSELFPGGSTRDLQ 692
QY 649 BEETQKAACKSLPCARNLAHAFYQFAPLILQSHAKAIVILVRLGALGLSLYGATLVQ 708
Db 693 LDESKEKRECVPLPFLKWSLSDFAREKAPVLLKAEKIGIVVAFMALLGLGLYGTVMV 752
QY 709 DGLALTDVVRGTKEHAFSLAOLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRPSSLKA 768
Db 753 DGLYLTIDIPRETKEYNFISAFKFSFYNFIVTKDGNYPKQESLYDLHEAFSGSVRY 812
QY 769 VLPPTAQAPRWLHYRNWLOGIAQAFDQDQWASGRITRHSYRNSEDCGALAYKLLIQTG 828
Db 813 VVREGRDLPKMLHYFQDLWRLGLQTFADKOWESGRMTQDNYRNGTGDGLYKLLIQTG 872
QY 829 DAQEPDLFSQTLTKLVDRGELIPPELFVMTGLTVVWSSDPLGLAASQANFYPPPEWUHD 888
Db 873 NKKEPFNFNQLTSRLVDEKGLPQDAFYIYLTVMVNSNDPLGYAASQANFYPPPEWUHD 932
QY 889 KYDTTGENLRIPPAOLPEFAQPELLRGLOKTDVFEATEGARACAEAGQGVHAYPSG 948
Db 933 RYDTTGENLRIPPAOLPEFAQPELLRGLOKTDVFEATEGARACAEAGQGVHAYPSG 992
QY 949 SPFLFEWQYGLRRCFLLAVCILLVCTFLVACALLLNPMWTAGLIVLVLAMMTVELFGMG 1008
Db 993 YPFLFEWQYGLRRCFLLAVCILLVCTFLVACALLLNPMWTAGLIVLVLAMMTVELFGMG 1052
QY 1009 FIGIKLSAIPVVLVAVSGIVGVEFTVHVALGFLTTQSGRNLRRAAHLEHTFAPVTDGAS 1068
Db 1053 LTIGIKLSAIPVVLVAVSGIVGVEFTVHVALGFLTTQSGRNLRRAAHLEHTFAPVTDGAS 1112
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QY 1069 TLLGLMLAGSHFDRIYRVFFAALTVLTLGLLHGLVLLPVLILGPPPEVI-----Q 1122
Db 1113 TLLGLVLMAGSBFDRIYRVFFAALTVLTLGLLHGLVLLPVLILGPPPEVI-----Q 1172
QY 1123 MYKESPEILSPAPQGGGLRWGASSSLPOS----FARVTTMTVAIHPPEL--PGAYIHP 1176
Db 1173 LPTTPEPLPPLSHHAFYMNHKGSDPDSSEYSEYSEITTTSGLEDDPRLYERSAYI-- 1230
QY 1177 APDEPP 1182
Db 1231 IPPKPP 1236
```

RESULT 9
AAH70995 PRELIMINARY; PRT; 1422 AA.
AC AAH70995, (TREMREL. 27, Created)
DT 24-MAY-2004 (TREMREL. 27, Last sequence update)
DT 24-MAY-2004 (TREMREL. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.L., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070995; AAH70995.1; --
KW Hypothetical protein.
SQ SEQUENCE 1422 AA; 159128 MW; 28842656E60CE72 CRC64;

Query Match 65.5%; Score 4106; DB 2; Length 1422;
Best Local Similarity 65.3%; Pred. No. 7,9e-267;
Matches 787; Conservative 165; Mismatches 215; Indels 39; Gaps 9;

QY 12 PSYTPARTAAPOILAGSL---KAPLWLRAYFOGLLFSLGCGTQORHCGKVFLGLLAFGA 68

RT hedgehog and maps to a region associated with developmental
 RT abnormalities.";
 RL J. Biol. Chem. 271:12125-12128(1996).
 RN [3]
 RN VARIANTS BCNS ARG-509; VAL-509; GLN-816 DEL AND TYR-1132.
 RX MEDLINE=96438609; PubMed=8840969;
 RA Chidambaram A., Goldstein A.M., Gailani M.R., Gerrard B., Bale S.J.,
 RA DiGiovanna J.J., Bale A.E., Dean M.;
 RA "Mutations in the human homologue of the Drosophila patched gene in
 RT Caucasian and African-American nevoid basal cell carcinoma syndrome
 RT patients.";
 RL Cancer Res. 56:4599-4601(1996).
 RN [4]
 RN VARIANTS BCNS TYR-513 AND ARG-1069.
 RX MEDLINE=97136566; PubMed=8981943;
 RA Wicking C., Shanley S., Smyth I., Gillies S., Negus K., Graham S.,
 RA Suthers G., Hailes N., Edwards M., Wainwright B.J.,
 RA Chenevix-Trench G.;
 RA "Most germ-line mutations in the nevoid basal cell carcinoma syndrome
 RT lead to a premature terminations of the PATCHED protein, and no
 RT genotype-phenotype correlations are evident.";
 RL Am. J. Hum. Genet. 60:21-26(1997).
 RN [5]
 RN VARIANT NBCCS ASP-1438.
 RX MEDLINE=98001068; PubMed=9341860;
 RA Lench N.J., Telford E.A.R., High A.S., Markham A.F., Wicking C.,
 RA Wainwright B.J.;
 RA "Characterisation of human patched germ line mutations in naevoid
 RT basal cell carcinoma syndrome.";
 RL Hum. Genet. 100:497-502(1997).
 RN [6]
 RN VARIANT PRO-1315.
 RX MEDLINE=99211211; PubMed=10200051;
 RX DOI=10.1002/(SICI)1098-1004(1998)11:6<480::AID-HUMU9>3.3.CO;2-W;
 RA Hasenpuesch-Thell K., Bataille V., Laehdetie J., Obermayr F.,
 RA Sampson J.R., Frischauf A.-M.;
 RA "Corlin syndrome: identification of 4 novel germ-line mutations of the
 RT human patched (PTCH) gene.";
 RL Hum. Mutat. 11:480-480(1998).
 RN [7]
 RN VARIANTS BCNS SER-376 AND VAL-1083 INS, AND VARIANT BCC TRP-1114.
 RX MEDLINE=98281604; PubMed=9620294;
 RA Aszterbaum M., Rothman A.L., Johnson R.L., Fisher M., Xie J.,
 RA Bonifas J.M., Zhang X., Scott M.P., Epstein E.H. Jr.;
 RA "Identification of mutations in the human PATCHED gene in sporadic
 RT basal cell carcinomas and in patients with the basal cell nevus
 RT syndrome.";
 RL J. Invest. Dermatol. 110:885-888(1998).
 RN [8]
 RN VARIANT PRO-1315.
 RX MEDLINE=20334946; PubMed=10874314;
 RX DOI=10.1002/1098-1004(200007)16:1<89::AID-HUMU18>3.3.CO;2-Z;
 RA Dong J., Gailani M.R., Pomeroy S.L., Reardon D., Bale A.E.;
 RA "Identification of PATCHED mutations in medulloblastomas by direct
 RT sequencing.";
 RL Hum. Mutat. 16:89-90(2000).
 RN [9]
 RN VARIANT BCNS PRO-1132.
 RX MEDLINE=21154106; PubMed=11231326;
 RA Reifemberger J., Arnold N., Kiechle M., Reifemberger G., Hauschild A.;
 RA "Coincident PTCH and BRCA1 germline mutations in a patient with nevoid
 RT basal cell carcinoma syndrome and familial breast cancer.";
 RL J. Invest. Dermatol. 116:472-474(2001).
 RN [10]
 RN VARIANTS SQUAMOUS CELL CARCINOMA MET-829 AND LYS-1242.
 RX MEDLINE=21184537; PubMed=11286632;
 RA Ping X.L., Ratner D., Zhang H., Wu X.L., Zhang M.J., Chen F.F.,
 RA Silvers D.N., Peacocke M., Tsou H.C.;
 RA "PTCH mutations in squamous cell carcinoma of the skin.";
 RT J. Invest. Dermatol. 116:614-616(2001).
 RL CC -1- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
 CC hedgehog (IHH) and desert hedgehog (DHH). Associates with the
 CC smoothened protein (SMO) to transduce the hedgehog's proteins

CC signal. Seems to have a tumor suppressor function, as inactivation
 CC of this protein is probably a necessary, if not sufficient step
 CC for tumorigenesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: In the adult, expressed in brain, lung, liver,
 CC heart, placenta, skeletal muscle, pancreas and kidney. Expressed
 CC in tumor cells but not in normal skin.
 CC -1- DEVELOPMENTAL STAGE: In the embryo, found in all major target
 CC tissues of sonic hedgehog, such as the ventral neural tube,
 CC somites, and tissues surrounding the zone of polarizing activity
 CC of the limb bud.
 CC -1- PTM: Glycosylation is necessary for SHH binding (By similarity).
 CC -1- DISEASE: Defects in PTCH are probably the cause of basal cell
 CC nevus syndrome (BCNS) [MIM:109400]; also known as Gorlin syndrome
 CC or Gorlin-Goltz syndrome. BCNS is an autosomal dominant disease
 CC characterized by nevoid basal cell carcinomas (NBCCS) and
 CC developmental abnormalities such as rib and craniofacial
 CC alterations, polydactyly, syndactyly, and spina bifida. In
 CC addition, the patients suffer from a multitude of tumors like
 CC basal cell carcinomas (BCC), fibromas of the ovaries and heart,
 CC cysts of the skin, jaws and mesentery, as well as medulloblastomas
 CC and meningiomas. PTCH is also mutated in squamous cell carcinoma
 CC (SCC). Could also be associated with large body size observed in
 CC BCNS patients.
 CC -1- DISEASE: Defects in PTCH are a cause of sporadic basal cell
 CC carcinoma (BCC) [MIM:605462].
 CC -1- SIMILARITY: Belongs to the patched family.
 CC -1- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
 CC -1- DATABASE: NAME=PTCH mutation database;
 CC WWW="http://www.cybergene.se/PTCH/ptchbase.html".
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PTCH100.html".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U59464; AAC50550.1; -;
 CC EMBL; U43148; AAC50496.1; -;
 CC Genew; HGNC:9585; PTCH.
 CC MIM; 601309; -;
 CC MIM; 109400; -;
 CC MIM; 605462; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004872; P:receptor activity; TAS.
 CC GO; GO:0008283; P:cell proliferation; TAS.
 CC GO; GO:0009653; P:morphogenesis; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR004766; Patchedtm_recept.
 CC InterPro; IPR000731; SSD 5TM.
 CC Pfam; PF02450; Patched; 1.
 CC TIGRFAMs; TIGR00918; 2A060602; 1.
 CC PROSITE; PS50156; SSD; 1.
 CC Anti-oncogene; Disease mutation; Glycoprotein; Polymorphism; Receptor;
 KW Transmembrane.
 FT DOMAIN 1 100 Cytoplasmic (Potential).
 FT TRANSMEM 101 121 Potential.
 FT DOMAIN 122 436 Extracellular (Potential).
 FT TRANSMEM 437 457 Potential.
 FT DOMAIN 458 472 Cytoplasmic (Potential).
 FT TRANSMEM 473 493 Potential.
 FT DOMAIN 494 501 Extracellular (Potential).
 FT TRANSMEM 502 522 Potential.
 FT DOMAIN 523 547 Cytoplasmic (Potential).
 FT TRANSMEM 548 568 Potential.
 FT DOMAIN 569 577 Extracellular (Potential).
 FT TRANSMEM 578 598 Potential.
 FT DOMAIN 599 748 Cytoplasmic (Potential).

FT	TRANSMEM	749	769	Potential.	
FT	DOMAIN	770	1027	Extracellular (Potential).	
FT	TRANSMEM	1028	1048	Potential.	
FT	DOMAIN	1049	1055	Cytoplasmic (Potential).	
FT	TRANSMEM	1056	1076	Potential.	
FT	DOMAIN	1077	1083	Extracellular (Potential).	
FT	TRANSMEM	1084	1104	Potential.	
FT	DOMAIN	1105	1121	Cytoplasmic (Potential).	
FT	TRANSMEM	1122	1141	Potential.	
FT	DOMAIN	1142	1154	Extracellular (Potential).	
FT	TRANSMEM	1155	1175	Potential.	
FT	DOMAIN	1176	1447	Cytoplasmic (Potential).	
FT	DOMAIN	14	31	Gly-rich.	
FT	TRANSMEM	438	598	SSD.	
FT	CARBOHYD	141	141	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	312	312	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	349	349	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	414	414	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	875	875	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	1000	1000	N-linked (GlcNAc. . .) (Potential).	
FT	VARIANT	175	175	L -> P (in BCNS; sporadic BCC).	
FT	VARIANT	376	376	/FTID=VAR_007843.	
FT	VARIANT	509	509	F -> S (in BCNS).	
FT	VARIANT	509	509	/FTID=VAR_007844.	
FT	VARIANT	509	509	G -> R (in BCNS; could be a rare	
Query Match					
Best Local Similarity					53.4%; Score 3348; DB 1; Length 1447;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;					
QY	12	PSYTPPARTAAPOILAGSL	---KAPLMRLAYFQGLLPSLGGIORHCGKVLFLGLAFGA	68	
DB	53	PSYC-DAFALEQISGKATGRKAPLMRLAKFORLLFKGLCYIQNKQKFLVWGLIFGA	111		
QY	69	LALGLRMAIETNLBQLWVEGSRVSOELHYTKREKLGEAAAYTSOMLIQTARQGENILT	128		
DB	112	FAVGLKAANLETNVEELWVEGSRVRELNYTRQKIGEEAMFNQPMIQTPEEGANVLT	171		
QY	129	PEALGLHQAALTASKVOVSLYKGSWDLNKKI CVKGVPLIENGMIEMIEKLPFCVILTP	188		
DB	172	TEALLQHLDSALQASRVHVMYNNRWKLEHLCKVSGELITETGYMDQIIIEYLYPCLIIPT	231		
QY	189	LDCFEGAKLQGSAYLPCRPDIQWNTLDPQLLEELPGF-ASLEGFRELLDKAQVGQAY	247		
DB	232	LDCFEGAKLQSGTAYLLGKPLRWTFNPDLPFLFLEELKKINYQVDSWEEMLNKAEVGHGY	291		
QY	248	VGRPCILHPDDLCPSPAPNHHSRQAPNVAHELSGCHGFSKFMHQEBELLGGMARDPQ	307		
DB	292	MDRPCINPADPCPATAPNKNSTKPLDMALVNGGCHGLSRKYMHWQELIIVGTVKNST	351		
QY	308	GELLRAEALQSTFLMSRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA	366		
DB	352	GKLVSHAALQTMFQMLTPKQMYEHFKGYEVSH-INWNEDKAAAILAEAWQTYVEVWHQS	410		
QY	367	LPEASQOIHAFSSYTLDDILHAFSEVSAARVVGVLMLAYACTVMTLWDCACQSGSVG	426		
DB	411	VQNSTQKVLSTFTTLDDILKLSFSDSVIRVASGYLLMLAYACTVMTLWDCACSQGAVG	470		
QY	427	LAGVLLVALAVASGLGCLALLGTTFNAATQVLPFLALGIGVDVDFLLAHAFTEALPG--	484		
DB	471	LAGVLLVALVAAGLGCLSLIGISFNAAATQVLPFLALGVGVDVDFLLAHAFSETQNKR	530		
QY	485	TPLOERMGCECLQRTGTSVVLTSINNMAAFMAALVIPALRAFSQAALIVGCTFVAVML	544		
DB	531	IPFEDRTGCECLKRTGASVALTSISNTAFMAALIPALRAFSQAALVAVVFNFAVMVL	590		
QY	545	VFPAILSLDLRRHRCQRLVDLCFSSPCSAQVILQILPQELGD-----GTPVPGIAH--	595		
DB	591	IPFALLSMOLYRRDRRLDIFCCTSPCVSRVQIPEQAYTHTDNTFYSPPPVSSHFS	650		
QY	596	-----LTAATVQAFHCEASSQHVVTILPQAHLVPPP-----SDPLGSELFSFGGSTRD	644		
DB	651	AHETQITQMSTVOLRTEYDPHTVVYTTAEPRSEISVQPVVTQDTLSCQSPESSTSP	710		

QY	645	LLGQEEETROKAAKSKSLPCARWNLAHFARYQAPLILQSHAKAIVLVLPGLLGLSLYGA	704	
DB	711	LLSQFSDS--SLHCLPEPCTKTWLTSSFAEKHYAPFLKPKAKVWVIFLFLGLGLVSLYGT	768	
QY	705	TLVQDGLALTVDVVRGTKEHAFSLAQRLYFSLYEVALVTQGGFDVAHSORALFDLHOREFS	764	
DB	769	TRVRDGLDLDIVPRETREYDFIAAQFKYFSYNNMIIVTQKA-DYPNIQHLIYDLHRSFS	827	
QY	765	SLKAVLPPPATQAPRTWLYHRYNNWLGQIAAFDQDQWASGRITRHSYRNGSEDCALAYKIL	824	
DB	828	NVKYVWLEENKQLPKMWLHYPRDMLQGLQDAFDSDMETGKIMNNVKNKSGDDGVLAYKLL	887	
QY	825	IOTGAQAPLDPFSQLTTRKLVDRREGLIPPELPMGLTVMWSSDPLGLAASQANFPPTTPE	884	
DB	888	VOTGSRDKPIDISQLTQKRLVDADGIINPSAFYIYLTAWVSDPVAYASQANIRPHRE	947	
QY	885	WLHDKYDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADEFVIAEGARAAEAGQAGVH	943	
DB	948	WVHDKADYWPETRLRIPAAEPIEYAFPPYLNGLRDTSDTDFEAIKVRTICSNYISLGLS	1007	
QY	944	AYPSGSPFLFWBQYLGRLRCFLAVCIILVCTFLVCALLLNPNWTAGLIVLVLMMTVEL	1003	
DB	1008	SYPNGYPFLFWBQYIGRLHLLFIISVLAFTLVCAVFLNPNWTAGIIVVLMMTVEL	1067	
QY	1004	FGIMFLGKLSAIPWVILVASVGVGERTVVAFLGTLTQGSRLRAHALEHTFAPVT	1063	
DB	1068	FGMMLIGIKLSAVPWVILIASVGVGERTVVAFLGTLTQGSRLRAHALEHTFAPVT	1127	
QY	1064	DCAITLGLMLAGSHDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1121	
DB	1128	DCAVSTLGLVLMAGSEDFIVRYFFAVLAITLITGLVNLGLVLLPVLISILGPPPEVSPA	1187	
QY	1122	-----QMYKESP-----ILSP-----APOG 1139		
DB	1188	NGLNRLPTSPRPVVRFPMPGTHSGSDSDSEYSSQTTVSGLSSELRHYEAQQA	1247	
QY	1140	G-----LRWG-----ASSLPGSFAR 1155		
DB	1248	GGPAQVIVEATENPVFAHSTVVPESRHHPPSNRQOPHLDSGLSPGRQOQRRDPP	1307	
QY	1156	VTT-----SMTVAIHPPPLPGYIHP 1176		
DB	1368	ITVTASASVTVAVHPPPVPGGRNP 1393		
RESULT 12				
QY	Q90XB9	PRELIMINARY;	PRT;	913 AA.
ID	Q90XB9	PRELIMINARY;	PRT;	913 AA.
AC	Q90XB9	PRELIMINARY;	PRT;	913 AA.
DT	01-DEC-2001	(Tremblrel. 19, Created)		
DT	01-DEC-2001	(Tremblrel. 19, Last sequence update)		
DT	01-OCT-2003	(Tremblrel. 25, Last annotation update)		
DE	Patched 2	(Fragment)		
GN	Name=PTC2;			
OS	Gallus gallus (Chicken)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus			
OK	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Pearse R.V. Jr., Vogan K.J., Tabin C.J.;			
RT	"Ptc1 and Ptc2 transcripts provide distinct readouts of Hedgehog			
RT	signaling activity during chick embryogenesis."			
RL	Dev. Biol. 0:0-0(2001).			
DR	EMBL; AF409095; AAK97655.1; --			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0008158; F:hedgehog receptor activity; IEA.			


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FT TRANSMEM 473 493 Potential.
FT DOMAIN 494 501 Extracellular (Potential).
FT TRANSMEM 502 522 Potential.
FT DOMAIN 523 547 Cytoplasmic (Potential).
FT TRANSMEM 548 568 Potential.
FT DOMAIN 569 577 Extracellular (Potential).
FT TRANSMEM 578 598 Potential.
FT DOMAIN 599 747 Cytoplasmic (Potential).
FT TRANSMEM 748 768 Potential.
FT DOMAIN 769 1026 Extracellular (Potential).
FT TRANSMEM 1027 1047 Potential.
FT DOMAIN 1048 1053 Cytoplasmic (Potential).
FT TRANSMEM 1054 1074 Potential.
FT DOMAIN 1075 1082 Extracellular (Potential).
FT TRANSMEM 1083 1101 Potential.
FT DOMAIN 1102 1120 Cytoplasmic (Potential).
FT TRANSMEM 1121 1141 Potential.
FT DOMAIN 1142 1153 Extracellular (Potential).
FT TRANSMEM 1154 1174 Potential.
FT DOMAIN 1175 1442 Cytoplasmic (Potential).
FT TRANSMEM 1443 160577 MW; 973E5F17FB8B6E43 CRC64;
FT CARBOHYD 141 141 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 312 312 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 349 349 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 414 414 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 827 827 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 874 874 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 999 999 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 1442 AA; 160577 MW; 973E5F17FB8B6E43 CRC64;

Query Match 53.3%; Score 3340; DB 1; Length 1442;
Best Local Similarity 54.3%; Pred. No. 2.6e-215; Indels 50; Gaps 17;
Matches 663; Conservative 204; Mismatches 304;

QY 12 PSYTPARTAAQIILAG---SLKAPLWLRAYFQGLLFSLCGGIQRHCGKVLFLGLAFA 68
DB 54 PSYC-DAAPALQIAKGRATGRAPLWLRKQRULLFNLGCIYQKNGKFLVUGLL-YSA 111

QY 69 LALGLRMAIENLEQLWVEGSRVSELYKKEGEEAAYTSQMLIOTARQEGENILT 128
DB 112 FAVGLRAANLETVNELWVEGSRVSELYKKEGEEAAYTSQMLIOTARQEGENILT 171

QY 129 PEALGLHQAALTASKVQVSLYKGSWDANKICVKGVPILJENGMIEMMLEKFLPCVILT 188
DB 172 TEALQKHLDSALQAKGRVHYMYNRQKLEHLCYKSGELITEAGYMDPILEYLPCLIITP 231

QY 189 LDCFMEGAKLQGSAYLPGRDPIQWNLDPQLLEELGPF-ASLEGFRELLEKAAQVGQAY 247
DB 232 LDCFMEGAKLQGSAYLLGKPPPLQWINFDPLELEELKKINYQVESWEEMLNKAEVGHY 291

QY 248 VGRPCLPEDDLHCPPSAPNHHSRQAPNVAHELSCGCHGSHKFMHQBELLILGWARDPQ 307
DB 292 MDRPCLPNADPDCPTAPNKNSTKPLDVALVLSGGCYGLSRKYMHWQEBLLIGGTVKNS 351

QY 308 GELLRAEALQSTFLMSRQLYEHFRG-DYOTHDIGWSEEQASTVLOAQRFRVQLAQR 366
DB 352 GKLVSAQAQLQWFLMTPKQMEHFYGVSH-INWNEKKAAILLEAQRMYVEVHOS 410

QY 367 LPENASQIHAFSSTTLDILHAFSFSVAARVVGGYLLMLAYACVTMLRWDCAQSGSVG 426
DB 411 VAQNSTQKVLSTFTTTLDILKLSFSDSVIRVASGYLLMLAYACVTMLRWDCAQSGAVG 470

QY 427 LAGVLLVALAVASGLGCLLGLITFNAAATQVLPFLALGIVDDVFLLAHATEALPG-- 484
DB 471 LAGVLLVALAVASGLGCLLGLITFNAAATQVLPFLALGIVDDVFLLAHATEALPG-- 530

QY 485 TPLQERMGCLORTGTSVVLTSNNMAAFMLAALVPIPALRAFSLOAAIVGCTFFAVML 544
DB 531 IFPEDRTGCLKRTGASVALTSISNVTAFPMALIPALRAFSLOAAIVVFNFAVML 590

QY 545 VFPAILSLDRRRHCRQLDVLCCFSFSCSAQVITQILPQELGD-----GTVPVGLAH--- 595
DB 591 IFPAILSMDLRYRDRRLDIFCCFTSPCTVRIQIEPQAYEAENDNICYSSPPYSSHPA 650

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QY 596 -----LRTAQAFTHCEASSQHVVITLPPQAHLYPPP-----SDPLGSELFPGGSTRDL 645
DB 651 HETQITMSTVQLRTEYDPHTQAYTTTAEPRSEISVQPVTVTQDSLSCQSPESASSTRDL 710
QY 646 LQGEETRQKAACKSLPCARWMLAHFARYQFAPLLOSHAKAIVLVLFQALLGLSLYGAT 705
DB 711 LSQFSDS--SVHCLEPPCTKWTLSFAEKHYAPFLPKRAKVUVIFLGLGLSLYGT 768
QY 706 LVQDGLALTDDVVPRTGKEHAFSLAQLRYFSLYEVALVTQGGFDYAHQSRALEDLHORFSS 765
DB 769 RVRDGLDLTDIVPRTREYDFIAAQFKYFSEYNNMIVTQKA-DYENVQHLLEHRSFSN 827
QY 766 LKAVLPPPATQAPRTWLHYRNWLOGIAAFQDQWASGRITHSRHSRNGSEDEGALAYKLII 825
DB 828 VTYVLEGGDRQLPKMWLHYFRDLWGLQDAFDSWETGKITYSNYKNGSDDAVLAYKLIV 887
QY 826 QTGDAQEPDLFSQLTTRKLVDRREGILPPELFYMGLTVMVYSSDPLGLAASQANFYPPPEW 885
DB 888 QTGNRAKPIDISQLTQRKQRLVDADGIINPNAFYILTAMVNSDPVAYASQANIRPHRPEW 947
QY 886 LHDKYDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADFEVAIEGARAAACABAGQAGVHA 944
DB 948 VHDKADYMPETRLRIPAAEPIEYAOFPFYNGLRRETSDFEVALEKVRACNNVYSLGIAS 1007
QY 945 YPSGSPFFLFWEOYLGLRRCFLAVCLLVCTFLVCALLLNPTWAGLIVLVLAMTVLELF 1004
DB 1008 YPNGYPFLFWEOYIGLRHMLLSISVLACTFLVCALFLNPNWTAGIIVVVLALMTVELE 1067
QY 1005 GIMGFLGIKLSAIPVILVASVIGVEFTVHVVALGFLTTOGSRNLRAAHALHTTAPVTD 1064
DB 1068 GMMGLIGIKLSAVPVVILLASVIGVEFTVHVVALGFLTTOGSRNLRAAHALHTTAPVTD 1127
QY 1065 GAISTLLGLMLAGSHDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSLILGPPPEVI--- 1121
DB 1128 GAVSTLLGLVLAGSEDFIVRYFFAVLAILITLGLVINGLVLVLLPVLLSFFGYPPEVSPAC 1187
QY 1122 ---QMKYSPELSPPA-----POGGGLRWGASSLPSOSFARVTTSMVAIH---PPPL 1169
DB 1188 GRNLFTPSPE--PPFSIVRFALPFGHTNNGSDSDSEYSSQTTVSGISELHHEATQS 1245
QY 1170 PGAYTHPAPDEPPWSPAATSS 1190
DB 1246 PGIPVHVQVVEATENPVFARS 1266

RESULT 14
Q6UY90 PRELIMINARY; PRT; 1434 AA.
AC Q6UY90;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Patched.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P344;
RX MEDLINE=22381811; PubMed=12469128;
RA Lai K., Kaspar B.K., Gage F.H., Schaffer D.V.;
RT "Sonic hedgehog regulates adult neural progenitor proliferation in
RT vitro and in vivo.";
RL Nat. Neurosci. 6:21-27(2003).
DR EMBL; AY357891; BAA067738.1;
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patched.
DR Pfam; PF02460; Patched; 1.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.

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Qy	416	WDCAQSGSVGLAGVLLVALAVASGLGICALLGHTFNAAATQVLPFLIAGLVDDVPFLA	475
Db	446	WDCSKQAGVLAGVLLVALSVAGLGLICLIGISFNAATQVLPFLIAGLVDDVPFLA	505
Qy	476	HAFTEALPG--TPLOERMGECIORTGTSVVLTSINNMAAFMLMAALVPDIPALRAFSLOAAI	533
Db	506	HAFSETQNKRIPEPDTGTECLKKTGASVALTSLNVTAFMAALDIPALRAFSLOQAV	565
Qy	534	VWGCTFVAVMLVPFALLSLDLRRRHQCQLDVLCCFSSPCSAQVITQILPQELGDTVP---	590
Db	566	VVVFNFAMVLLIPFALLSMDLYRREDRLDIFCCFTSPCVSRVIVQEPQAV---TEPHSN	622
Qy	591	-----VGIAHUT-----ATVQAFTHCEASSOHVVTILPPQAHLVPPP-----SDP	630
Db	623	TRYSPPPPPYSGSHSPAHEHTHIMQSTQVLRTEYDPTHVTYVTTAEPSEISVQPVITQDT	682
Qy	631	LGSELFPGGSTRDLLGQEBETROKAAKSLPCARWNLAHFARYQFAPLPLLQSHAKAIVL	690
Db	683	LSCSPSTSTRDLLSQFSDS--SLHCLPPTCKWTLSLSEAKHYAPFLLRPKAKVVVI	740
Qy	691	VLFGALLGLSLYGATLVODGLALTDDVVPRTGKEHAFLSAQLRVPSLYEVALVTQGGDYA	750
Db	741	LLFLGLAGVSLYGTTRVDRGLDLTDIVERETREYDFIAAQKYPSPFNMVIVTQKA-DYP	799
Qy	751	HSQPAFLDLHQRESSLKAIVLPPPATQAPRTWLHYRNWLOGIQAAQPDQWASGREITHSY	810
Db	800	NIQHLLYDLHKSPSSVKYVMLEENKQUPQMWLHYFRDWLQLODAFDSQWETGRIMPNNY	859
Qy	811	RNGSEDGALAYKLLIQTGDAQEPDLDFSQLTRKLVDRGLPIPELFFYMGLTIVWVSSDPLG	870
Db	860	KNGSDDGVLAYKLLVQTSRDKPIDISQTKQRLVDADGIINPSAFIYILTAWWSNDPVA	919
Qy	871	LASQANFYPPPBWLHDKYDTTGE-NIRTPPQPLEPFAQFPFLLRGLQKTAQDFVEAIEG	929
Db	920	YAASQANIRHRPEWVHDKADYMETRLRIPAAEFIEYAQFPFYNLGRDTSDFVEAIEK	979
Qy	930	ARAAACBAGQAGVHAYPSGSPFFLWEOYVGLRRCFLIACVILICVCTFLVCALLLNWPWA	989
Db	980	VRVICNNYTSIGLSSYNGPFFLEWEOYISLRHWLLLAISVULACTFLVCVALLNWPWA	1039
Qy	990	GLIVLVLAMTMVELFGIMFGLIKLSAIPVVILVASVIGVGEFTVHVALGFLTQGSRNLL	1049
Db	1040	GIIVWVLAJMTVELFGMWGLIGIKLSAVPVVILLIASVIGVGEFTVHVALAFLTAIGDKNH	1099
Qy	1050	RAAHLEHTAPVTDGAI STLGLLLMAGSHDFIVRYFPAALTVLTLGLLHGLVLLPV	1109
Db	1100	RAMIALEHMFAPVLDGAVSTLLGVIMLAGSEDFIVRYFPAVLAJLTVLGVINGLVLPPV	1159
Qy	1110	LLSLTGLPPEPVIQWYKESPEILSPPAQGGGLRWGASSSLPQSFARVTTSMTVAIHPPL	1169
Db	1160	LLSFFGCPPEV-----SPANG-----INRLP-----TSPPEPPS	1189
Qy	1170	PGAYIHPADPPWSPAAATSGNLSL	1195
Db	1190	WVFAFV-----PGHTNKGSDSS	1207

Search completed: November 22, 2004, 07:57:32
Job time : 99 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 05:38:23 ; Search time 78 Seconds

(without alignments)
5532.710 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPPLRELPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	6272	100.0	1203	2	AAY43261	Aay43261 Human pat
2	6272	100.0	1203	5	Aae19829	Aae19829 Human pat
3	6272	100.0	1203	6	ABG74104	Abg74104 Human pat
4	6248	99.6	1203	2	AAY28444	Aay28444 Human pat
5	6238	99.5	1203	3	AAY92703	Aay92703 Human pat
6	5911	94.2	1146	3	AAY92225	Aay92225 Human pat
7	5599	89.3	1182	5	AAE19831	Aae19831 Mouse pat
8	3348	53.4	1447	2	AAE19831	Aae19831 Mouse pat
9	3348	53.4	1447	2	AAW52200	Aaw52200 Human pat
10	3348	53.4	1447	2	AAW72969	Aaw72969 Human pat
11	3348	53.4	1447	4	AAE19829	Aae19829 Human pat
12	3348	53.4	1447	5	AAE19830	Aae19830 Human pat
13	3348	53.4	1447	5	ABJ10931	Abj10931 TRC8 rela
14	3348	53.4	1447	5	AAE19831	Aae19831 Mouse pat
15	3348	53.4	1447	5	AAE19831	Aae19831 Mouse pat
16	3348	53.4	1447	7	ABU62275	Abu62275 Human pat
17	3348	53.4	1447	7	ADD46678	Add46678 Human Pro
18	3348	53.4	1447	7	ADH62731	Adh62731 Human pat
19	3348	53.4	1447	8	ABE48989	Abe48989 Human pat
20	3337	53.2	1434	2	AAW52199	Aaw52199 Mouse pat
21	3337	53.2	1434	2	AAW72968	Aaw72968 Mouse pat
22	3337	53.2	1434	4	AAE19831	Aae19831 Mouse pat
23	3337	53.2	1434	5	AAE19831	Aae19831 Mouse pat
24	3337	53.2	1434	7	ABU62271	Abu62271 Mouse pat
25	3337	53.2	1434	7	ADE94215	Ade94215 Murine pt

ALIGNMENTS

RESULT 1

AA43261

ID AAY43261 standard; protein; 1203 AA.

XX AC AAY43261;

XX DT 19-JAN-2000 (first entry)

XX DE Human patched-2 protein sequence.

XX KW Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;

XX KW cell proliferation; cell differentiation; testicular cancer; gut disease;

XX KW degenerative disorder; nervous system disorder; Parkinson's disease;

XX KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;

XX KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;

XX KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;

XX KW therapy.

XX OS Homo sapiens.

XX PN WO9953058-A1.

XX PD 21-OCT-1999.

XX PF 02-APR-1999; 99WO-US007417.

XX PR 15-APR-1998; 98US-00060939.

XX PA (GETH) GENENTECH INC.

XX PI De Sauvage FJ, Carpenter DA;

XX DR WPI; 1999-620428/53.

XX PS N-PSDB; AAZ31717.

XX PT New isolated human patched-2 gene, used to develop products for treating,

XX PT e.g. cancer and Alzheimer's disease.

XX PS Claim 14; Fig 1; 124pp; English.

XX CC This sequence represents the human patched-2 (ptch-2) protein of the

XX CC invention. The patched-2 polypeptides are signalling molecules,

XX CC specifically for signalling and mediator molecules in the hedgehog (hh)

XX CC cascade which are involved in cell proliferation and differentiation.

XX CC They can be used for the treatment of disorders which are mediated at

XX CC least in part by Hh, especially Dhh, e.g. testicular cancer. They can

XX CC also be used for treating degenerative disorders of the nervous system,

XX CC e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou

Adh62722 Mouse pat
Ade48980 Mouse pat
Aar94380 Mouse pat
Aaw47157 Nevoid ba
Aaw82586 Human pat
Aaw52197 Precis co
Aaw72971 Precis co
Aab67156 Butterfly
Aag79573 Butterfly
Abu62149 Buckeye p
Ade94209 Peacock b
Adh62716 Butterfly
Ade48974 Butterfly
Abe59092 Drosophil
Abj10929 TRC8 rela
Aar86304 Drosophil
Aae05389 Human pat
Aab85751 Hedgehog
Aab31232 A consens
Abb79150 Patched p

CC Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug
 CC addiction. Patched-2 agonists can be used to treat gut diseases, bone
 CC diseases, skin diseases, diseases of the testis (including infertility),
 CC ulcers, lung diseases, diseases of the pancreas, diabetes, and
 CC osteoporosis. Antagonists or agonists of patched-2 may be used for
 CC treating disorders or creating a desirable physiological condition
 CC effected by blocking Hh signalling, especially Dhh signalling, e.g.
 CC contraception or infertility treatment. The products can also be used for
 CC detection, diagnosis, drug screening and production of transgenic animals
 XX

SQ Sequence 1203 AA;

Query Match 100.0%; Score 6272; DB 2; Length 1203;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLMRLAYFQGLLFLSGGIGIQRHCGKVL 60
 DB 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLMRLAYFQGLLFLSGGIGIQRHCGKVL 60

QY 61 LGLAFGALALGLRMAIIETNLEQLWVEGSRVSOELHYTKEKLGEEAAYSQMLIQTAR 120
 DB 61 LGLAFGALALGLRMAIIETNLEQLWVEGSRVSOELHYTKEKLGEEAAYSQMLIQTAR 120

QY 121 QGSENLTPDALGLHLQAALTASKQVSLYKSWDLNKKICYKSGVPLIENGMIEMIEKL 180
 DB 121 QGSENLTPDALGLHLQAALTASKQVSLYKSWDLNKKICYKSGVPLIENGMIEMIEKL 180

QY 181 FFCVILTPDLDFWEGAKLGGSAAYLFGRPDIQWTLNLDPEQLLEELGPFASLGSEFRELDDK 240
 DB 181 FFCVILTPDLDFWEGAKLGGSAAYLFGRPDIQWTLNLDPEQLLEELGPFASLGSEFRELDDK 240

QY 241 AQVGQAYVGRPCPLHPDDLHCPSAPNHHSRQAPNVAHELSCGCHGFSHKFMWQBELLLG 300
 DB 241 AQVGQAYVGRPCPLHPDDLHCPSAPNHHSRQAPNVAHELSCGCHGFSHKFMWQBELLLG 300

QY 301 GNARDPQGLLRRAELQSTFLMSPOLYHEHFRGDYQTHDQWSEBQASTVLQAWORRV 360
 DB 301 GNARDPQGLLRRAELQSTFLMSPOLYHEHFRGDYQTHDQWSEBQASTVLQAWORRV 360

QY 361 QLAQALPENASQIHAFFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCQA 420
 DB 361 QLAQALPENASQIHAFFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCQA 420

QY 421 SQSGVGLAGVLLVALAVASGLGLCALLGTTFNAAATQVLPFLALGIGVDDVFLLAHAFT 480
 DB 421 SQSGVGLAGVLLVALAVASGLGLCALLGTTFNAAATQVLPFLALGIGVDDVFLLAHAFT 480

QY 481 ALPGTPLQRMGECLORTGTSVVLTSINNMAFLMAALVPIPALRAFSLOAAIVVGCTFV 540
 DB 481 ALPGTPLQRMGECLORTGTSVVLTSINNMAFLMAALVPIPALRAFSLOAAIVVGCTFV 540

QY 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPSCSAQVIOILPQELGSGTVPVGIHAHTATV 600
 DB 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPSCSAQVIOILPQELGSGTVPVGIHAHTATV 600

QY 601 QAFTHCEASQHVVTILPQAHVLPVPPSPPLSGSELPSPGSTRDILGQEEETQKAAKCS 660
 DB 601 QAFTHCEASQHVVTILPQAHVLPVPPSPPLSGSELPSPGSTRDILGQEEETQKAAKCS 660

QY 661 LPCARNWLAHFARYQAPLILQSHAKAIVLVLFGALLGLSLYGATLVQDGLATDVVPRG 720
 DB 661 LPCARNWLAHFARYQAPLILQSHAKAIVLVLFGALLGLSLYGATLVQDGLATDVVPRG 720

QY 721 TXEHAFSLAQRYFSLYEVALVTQGGFDVAHSORALFDLHQRPSLSKAVLPPPATQAPRT 780
 DB 721 TXEHAFSLAQRYFSLYEVALVTQGGFDVAHSORALFDLHQRPSLSKAVLPPPATQAPRT 780

QY 781 WLHYENWLGIOQAAPDQWASGRITRHSYRNSEDGALAYKLLICTGDAQBELDPSQLT 840
 DB 781 WLHYENWLGIOQAAPDQWASGRITRHSYRNSEDGALAYKLLICTGDAQBELDPSQLT 840

QY 841 TRKLVDRGLIPPELFYMGILTVWVSDPLGLAASQANFYPPPEWLHDKYDITGTENLRIP 900

841 TRKLVDRGLIPPELFYMGILTVWVSDPLGLAASQANFYPPPEWLHDKYDITGTENLRIP 900
 QY 901 PAQPLEFAQFPPLRLGLQKTADFVEAIRGARAACAEAGQAGVHAYPSGSPFLFWQYIQL 960
 DB 901 PAQPLEFAQFPPLRLGLQKTADFVEAIRGARAACAEAGQAGVHAYPSGSPFLFWQYIQL 960

QY 961 RRCFLAVCIIILVCTFLVCALLLNPTAGLIVLVAMMTVELFGIMGFLGKLSAIPV 1020
 DB 961 RRCFLAVCIIILVCTFLVCALLLNPTAGLIVLVAMMTVELFGIMGFLGKLSAIPV 1020

QY 1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLLMAASH 1080
 DB 1021 ILVASVGIGVEFTVHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLLMAASH 1080

QY 1081 FDFIVRYFFAALTVTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGG 1140
 DB 1081 FDFIVRYFFAALTVTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGG 1140

QY 1141 LRWGASSLSLPOSFAVTTSMTVAIHPPLPGAYIHPAPDEPPWSPAATSSGNLSRGP 1200
 DB 1141 LRWGASSLSLPOSFAVTTSMTVAIHPPLPGAYIHPAPDEPPWSPAATSSGNLSRGP 1200

QY 1201 ATG 1203
 DB 1201 ATG 1203

RESULT 2
 AAE19829
 ID AAE19829 standard; protein; 1203 AA.
 XX AAE19829;
 XX 18-JUN-2002 (first entry)
 XX Human patched-2 (Ptc-2) protein.
 XX Human; patched-2; Ptc-2; cell proliferation; differentiation; therapy;
 KW Cytostatic; testicular cancer; hedgehog protein signalling.
 XX Homo sapiens.
 XX Key
 FH Domain Location/Qualifiers
 FT 57..76 /label= TM1
 FT /note= "Transmembrane domain"
 FT 394..414 /label= TM2
 FT /note= "Transmembrane domain"
 FT 427..449 /label= TM3
 FT /note= "Transmembrane domain"
 FT 458..477 /label= TM4
 FT /note= "Transmembrane domain"
 FT 502..524 /label= TM5
 FT /note= "Transmembrane domain"
 FT 532..553 /label= TM6
 FT /note= "Transmembrane domain"
 FT 687..705 /label= TM7
 FT /note= "Transmembrane domain"
 FT 964..984 /label= TM8
 FT /note= "Transmembrane domain"
 FT 988..1010 /label= TM9
 FT /note= "Transmembrane domain"
 FT 1014..1033 /label= TM10
 FT

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FT      /note= "Transmembrane domain"
FT      1058..1077
FT      /label= TM11
FT      /note= "Transmembrane domain"
FT      1091..1114
FT      /label= TM12
FT      /note= "Transmembrane domain"
XX      US6348575-B1.
PN      19-FEB-2002.
PD      15-APR-1999; 99US-00293505.
XX      15-APR-1998; 98US-0081884P.
PR      (GETH ) GENENTECH INC.
PA      De Sauvage F, Carpenter DA;
PI      WPI: 2002-215260/27.
XX      N-PSDB; AAD31576.
DR      Native human patched-2 polypeptide for treating disorders caused by
PT      Hedgehog protein signaling such as testicular cancer, and for screening
PT      cDNA libraries.
XX      Example 1; Fig 1; 82pp; English.
XX      The invention relates to an isolated sequence comprising a native human
CC      patched-2 (Ptc-2) polypeptide. The invention also relates to signalling
CC      and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC      cell proliferation and differentiation. The isolated sequence is useful
CC      for the treatment of disorders which are linked to Hedgehog, especially
CC      desert hedgehog expression, such as testicular cancer. It may also be
CC      used as a hybridisation probe in a cDNA library to isolate Ptc-2 or its
CC      homologues, and to diagnose whether a disorder is driven by Ptc-2 or
CC      Hedgehog protein signalling. The present sequence is human patched-2
CC      (Ptc-2) protein
XX      SQ      Sequence 1203 AA;

Query Match      100.0%; Score 6272; DB 5; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLCGIGRHCGRVLF 60
DB      1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLCGIGRHCGRVLF 60
QY      61 LGLLAFGALGLRMAIITNLEQLWVEVGRSVQELHYTKELGEEAAYSQMLIQIAR 120
DB      61 LGLLAFGALGLRMAIITNLEQLWVEVGRSVQELHYTKELGEEAAYSQMLIQIAR 120
QY      121 QEGENILTPALGLHLQAALTASKVQVSLYKGSMDLNKI CYKSGVPLIENGMIEMIEKL 180
DB      121 QEGENILTPALGLHLQAALTASKVQVSLYKGSMDLNKI CYKSGVPLIENGMIEMIEKL 180
QY      181 FPCVILTPDLCDFWEGAKLQGSAYLPGRPDIQTWNLDPELLELGPFASLGPRELLDK 240
DB      181 FPCVILTPDLCDFWEGAKLQGSAYLPGRPDIQTWNLDPELLELGPFASLGPRELLDK 240
QY      241 AQVGAYVGRPCLPDLDLHCCPSAPNHHSRQAPNVAAHLSGCGCHGFSKFMHWQBELLLG 300
DB      241 AQVGAYVGRPCLPDLDLHCCPSAPNHHSRQAPNVAAHLSGCGCHGFSKFMHWQBELLLG 300
QY      301 GMARDPQCELLRAEALQSTFLLMSRQLYEPRGDIQTHDIGWSEQAQSTVLQAWQRREV 360
DB      301 GMARDPQCELLRAEALQSTFLLMSRQLYEPRGDIQTHDIGWSEQAQSTVLQAWQRREV 360
QY      361 QLAQALPENASQOIHAFSSITLDDILHAFSEVSAARVVGGLMLAYACVTMLRWDCAQ 420
DB      361 QLAQALPENASQOIHAFSSITLDDILHAFSEVSAARVVGGLMLAYACVTMLRWDCAQ 420

OY      421 SQSSVGLAGVLLVALAVASGLGICALLGITFNAAITQVLPFLALGIGVDDVFLAHAFTE 480
DB      421 SQSSVGLAGVLLVALAVASGLGICALLGITFNAAITQVLPFLALGIGVDDVFLAHAFTE 480
QY      481 ALPGTPLQERMGECLQRTGTSVLTSSINMAAFMAALVPIIPALRAFSQAAIVVGCTFV 540
DB      481 ALPGTPLQERMGECLQRTGTSVLTSSINMAAFMAALVPIIPALRAFSQAAIVVGCTFV 540
QY      541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVQIQLPOELGDTGTVPGVIAHLTATV 600
DB      541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVQIQLPOELGDTGTVPGVIAHLTATV 600
QY      601 QAFTHCEASSQHVVTILPPQAHLVPPSPDPIGSELFSPGGSTRDLGQEEETRQKAACKS 660
DB      601 QAFTHCEASSQHVVTILPPQAHLVPPSPDPIGSELFSPGGSTRDLGQEEETRQKAACKS 660
QY      661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVLFQALLGLSLYGATLVODGLALTVDVVRG 720
DB      661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVLFQALLGLSLYGATLVODGLALTVDVVRG 720
QY      721 TKEHAFSLAQRYFSLYEVALVTQGFQDYAHQSQRALFDLHQRFSSILKAVLPPPAQAPT 780
DB      721 TKEHAFSLAQRYFSLYEVALVTQGFQDYAHQSQRALFDLHQRFSSILKAVLPPPAQAPT 780
QY      781 WLHYRNWLQGIQAAAFDQDQWASGRITRHSYRNGSEDEGALAYKLLIQTQDAQBPDPFSQLT 840
DB      781 WLHYRNWLQGIQAAAFDQDQWASGRITRHSYRNGSEDEGALAYKLLIQTQDAQBPDPFSQLT 840
QY      841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
DB      841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY      901 PAQPLEFAQFPFLRLGLQKTADFVEAIEGARACAEAGQAGVHAYPSGSPFLFWEOYLGL 960
DB      901 PAQPLEFAQFPFLRLGLQKTADFVEAIEGARACAEAGQAGVHAYPSGSPFLFWEOYLGL 960
QY      961 RRCFLAVCIILVCTFLVCALLLNPWTAGLIVLVLAMTVLVELFGIMFGIKLSAIPVV 1020
DB      961 RRCFLAVCIILVCTFLVCALLLNPWTAGLIVLVLAMTVLVELFGIMFGIKLSAIPVV 1020
QY      1021 ILVASVGIGVSTVHVALGELTQGSRLRAHALEHTFAPVTDCAISTLGLMLASH 1080
DB      1021 ILVASVGIGVSTVHVALGELTQGSRLRAHALEHTFAPVTDCAISTLGLMLASH 1080
QY      1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLSSILGPPPEVIQMYKESPEILSPAPQGGG 1140
DB      1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLSSILGPPPEVIQMYKESPEILSPAPQGGG 1140
QY      1141 LRWGASSSLPOSFARVTTMTVAIHPPPLPGAYIHPADDEPPWSPAATSSGNLSRGPGP 1200
DB      1141 LRWGASSSLPOSFARVTTMTVAIHPPPLPGAYIHPADDEPPWSPAATSSGNLSRGPGP 1200
QY      1201 ATG 1203
DB      1201 ATG 1203

RESULT 3
ABG74104
ID ABG74104 standard; protein; 1203 AA.
XX ABG74104;
AC ABG74104;
XX 02-APR-2003 (first entry)
XX Human patched-2 protein.
XX Human; patched-2; Dhh signalling; proliferation; differentiation;
KW chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
KW basal cell carcinoma; neurodegenerative disorder; memory deficit;
KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease;
KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;

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KW	bone disease; skin disease; testicular disease; ulcer; lung disease;
KW	pancreatic disease; diabetes; osteoporosis; desert hedgehog.
XX	Homo sapiens.
XX	US2002156245-A1.
XX	24-OCT-2002.
XX	20-NOV-2001; 2001US-00990046.
XX	15-APR-1998; 98US-0081884P.
PR	15-APR-1993; 99US-00293505.
XX	(GETH) GENENTECH INC.
XX	De Sauvage FJ, Carpenter DA;
XX	WPI: 2003-182650/18.
DR	N-PSDB; ABX15919.
DR	New nucleic acid, useful for manufacturing a medicament for diagnosing or
PT	treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
PT	e.g., testicular cancer.
XX	Claim 14; Fig 1; 85pp; English.
PS	The invention relates to a new isolated nucleic acid encoding a
CC	polypeptide having patched-2 biological activity, comprises DNA having at
CC	least 95% sequence identity with a DNA molecule or its complement
CC	encoding: (a) a human patched-2 polypeptide comprising the sequence
CC	ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
CC	Deposit No. 209778 designation). Also included are a vector comprising
CC	the nucleic acid, a host cell transformed with the vector, a process for
CC	producing patched-2 polypeptides, an isolated native sequence of human
CC	patched-2 polypeptide, a chimeric molecule comprising the vertebrate
CC	patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
CC	patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
CC	hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
CC	patched-2 that stimulates or enhances the normal functioning of patched-2
CC	in the Dhh signalling pathway, screening for ant/agonists of patched-2
CC	and diagnosing to determine whether a particular disorder is modulated
CC	The nucleic acid is useful for manufacturing a medicament for diagnosing
CC	or treating a disorder that is modulated by Dhh signalling e.g. tumour,
CC	basal cell carcinoma, neurodegenerative disorders, memory deficit,
CC	Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
CC	Huntington's disease, schizophrenia, stroke, drug addiction, gut
CC	diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
CC	diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
CC	Patched-2 may also be used to develop male contraceptives. The gene for
CC	Patched-2 is located on human chromosome 1p33-34. The present sequence
CC	represents human patched-2 protein
XX	Sequence 1203 AA;
SQ	Query Match 100.0%; Score 6272; DB 6; Length 1203;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MTRSPPLRLPPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLFLGCGIORHCKVLF 60
Db	1 MTRSPPLRLPPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLFLGCGIORHCKVLF 60
QY	61 LGLAFGALALGRMAIETNLEQLWVEVSGRSVQELHYTKEKLGEEAAYTSOMLIQTAR 120
Db	61 LGLAFGALALGRMAIETNLEQLWVEVSGRSVQELHYTKEKLGEEAAYTSOMLIQTAR 120
QY	121 QGENTLTPEALGLHQALATASKQVSLYKGSNDLNKICYKSGVPLIENGMIEMIEKL 180
Db	121 QGENTLTPEALGLHQALATASKQVSLYKGSNDLNKICYKSGVPLIENGMIEMIEKL 180
QY	181 FPCVILTPIDCFWEGAKLQGSAYLPGRPDQIOWTNLDPEQLLELGFASLEGFRELDDK 240
Db	181 FPCVILTPIDCFWEGAKLQGSAYLPGRPDQIOWTNLDPEQLLELGFASLEGFRELDDK 240

Db	181 FPCVILTPIDCFWEGAKLQGSAYLPGRPDQIOWTNLDPEQLLELGFASLEGFRELDDK 240
QY	241 AQVQAYVGRPCCLHPDDLHCPSPAPNHHSROAPNVAHELSCGCHGFSKFKMHWQBELLLG 300
Db	241 AQVQAYVGRPCCLHPDDLHCPSPAPNHHSROAPNVAHELSCGCHGFSKFKMHWQBELLLG 300
QY	301 GWARDPQGBELLRAEALQSTFELLMSPROLYEHFRGDIYQTHDIGWSEQASTVLQAWORRFV 360
Db	301 GWARDPQGBELLRAEALQSTFELLMSPROLYEHFRGDIYQTHDIGWSEQASTVLQAWORRFV 360
QY	361 QLAQEALPENASQOIHFASSTTDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
Db	361 QLAQEALPENASQOIHFASSTTDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
QY	421 SQSGVGLAGVLLVALAVASGLGCLCALLGITFNAATQVLPFLALGIGVDDVFLAHAFTE 480
Db	421 SQSGVGLAGVLLVALAVASGLGCLCALLGITFNAATQVLPFLALGIGVDDVFLAHAFTE 480
QY	481 ALPGTPLQERMGECLORTGTSVWLTSINMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
Db	481 ALPGTPLQERMGECLORTGTSVWLTSINMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
QY	541 AVMLVFPAILSLDLRRRHQRLDVLCCFSSPCSAQVIQILPOELGDTVPVGIHLTATV 600
Db	541 AVMLVFPAILSLDLRRRHQRLDVLCCFSSPCSAQVIQILPOELGDTVPVGIHLTATV 600
QY	601 QAFTHCEASSQHVVTILPQAHVLPSPDPLGSELFSFGSGSTRDILGQEEETROKAACKS 660
Db	601 QAFTHCEASSQHVVTILPQAHVLPSPDPLGSELFSFGSGSTRDILGQEEETROKAACKS 660
QY	661 LPCARWNLHAHFARYOFAPLLOQSHAKATVLPFGALLGLSLYGATLVQDGLALTVDVVRG 720
Db	661 LPCARWNLHAHFARYOFAPLLOQSHAKATVLPFGALLGLSLYGATLVQDGLALTVDVVRG 720
QY	721 TKHEAFLSAQLRFLSYEVALVTQGGFDYAHQSQRALFDLHQRFSLLKAVLPPTAQAPT 780
Db	721 TKHEAFLSAQLRFLSYEVALVTQGGFDYAHQSQRALFDLHQRFSLLKAVLPPTAQAPT 780
QY	781 WLHYRNWLMQTOAAFDQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQPLDPSQLT 840
Db	781 WLHYRNWLMQTOAAFDQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQPLDPSQLT 840
QY	841 TKRLVDREGLIPELFPYMGLTWVWSDPLGLAASQANFYPPPPPEWLHDKYDTTGENLRIP 900
Db	841 TKRLVDREGLIPELFPYMGLTWVWSDPLGLAASQANFYPPPPPEWLHDKYDTTGENLRIP 900
QY	901 PAQPLEFAQFPPELLRGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSGSPFLFWEOYLGL 960
Db	901 PAQPLEFAQFPPELLRGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSGSPFLFWEOYLGL 960
QY	961 RRCFLAVCILLVCTFLVCALLLLNFWTAGLVVLVLMNTVELFGIMGFLGKLSAIPV 1020
Db	961 RRCFLAVCILLVCTFLVCALLLLNFWTAGLVVLVLMNTVELFGIMGFLGKLSAIPV 1020
QY	1021 ILVAVSGVIGVEFTVHVALGFLTTCQSRNLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
Db	1021 ILVAVSGVIGVEFTVHVALGFLTTCQSRNLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
QY	1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
Db	1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
QY	1141 LWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPADPEPWSAATSSGNLSRGPGP 1200
Db	1141 LWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPADPEPWSAATSSGNLSRGPGP 1200
QY	1201 ATG 1203
Db	1201 ATG 1203

ID AAY28444 standard; protein; 1203 AA.
 AC AAY28444;
 XX
 DT 03-DEC-1999 (first entry)
 XX
 DE Human ptc-2 protein.
 XX
 KW Patched-2; ptc-2; human; hedgehog receptor; nontropic; neuroprotective;
 KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
 KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
 KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
 KW graft; transplant; treatment; nervous system injury; chemical injury;
 KW basal injury; infection; inflammatory; tumor-induced injury; ageing;
 KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
 KW Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis;
 KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
 KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
 KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
 KW lesion-induced death; neuron regeneration; damage repair; skeletal;
 KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
 KW prosthetic cartilage device; spermatogenesis; fertility enhancer.
 XX
 OS Homo sapiens.
 XX
 PN WO929854-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 08-DEC-1998; 98WO-US026009.
 XX
 PR 08-DEC-1997; 97US-0067940P.
 XX
 PA (ONTO-) ONTOGENY INC.
 XX
 PI Bumcrot DA;
 XX
 DR WPI; 1999-561298/47.
 DR N-PSDB; MAX89478.
 XX
 PT New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
 PT prevention and/or reduction of the severity of neurological conditions.
 PS Claim 3; Page 73-77; 80pp; English.
 CC
 CC This invention describes a novel recombinantly produced human patched-2
 CC (ptc-2) polypeptide which has nontropic, neuroprotective, cardiant,
 CC antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
 CC protein is a hedgehog receptor and is therefore capable of modulating
 CC hedgehog signalling, and so affect a number of hedgehog-mediated
 CC biological activities. The human patched-2 (ptc-2) protein can be used to
 CC screen for modulators, antagonists and agonists, which are likely to play
 CC an important role in the modulation of cellular proliferation and
 CC maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
 CC tissues during disease states. Modulators of ptc-2 protein can be used
 CC for in vivo reformation of tissue, to improve grafting and morphology of
 CC transplanted tissue; for the treatment, prevention and/or reduction of
 CC the severity of neurological conditions deriving from: injury to the
 CC nervous system including traumatic injury, chemical injury, vascular injury
 CC and deficits (such as ischemia resulting from stroke), together with
 CC infectious/inflammatory and tumor-induced injury; ageing of the nervous
 CC system including Alzheimer's disease; chronic neurodegenerative diseases
 CC of the nervous system including Parkinson's disease, Huntington's chorea,
 CC amyotrophic lateral sclerosis, as well as spinocerebellar degeneration;
 CC and chronic immunological diseases of the nervous system including
 CC multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
 CC of autonomic disorders of the peripheral nervous system, including
 CC disorders affecting the innervation of smooth muscle and endocrine
 CC tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
 CC Antagonists of ptc-2 protein can be used to prevent differentiation of
 CC cells in culture, as well as for treatment of chronic pain syndromes.
 CC Agonists may be used to rescue neurons from lesion-induced death as well
 CC as neuron regeneration, in diseases such CNS trauma infarction, (viral)

CC infection, metabolic disease, nutritional deficiency, toxic agents, and
 CC so on. ptc-2 therapeutics may also be used for the repair of central and
 CC peripheral nerve damage, for repair and regeneration of non-neuronal
 CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
 CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
 CC for generation of prosthetic cartilage devices, and to induce
 CC spermatogenesis and as fertility enhancers. This sequence represents the
 CC human ptc-2 protein described in the invention
 XX
 SQ Sequence 1203 AA;

Query Match 99.6%; Score 6248; DB 2; Length 1203;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRSPRLPSPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLPSLGGCIQRHCGKVLF 60

DB 1 MTRSPRLPSPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLPSLGGCIQRHCGKVLF 60

QY 61 LGLLAFGALALGLRMAIETNLEQLWVEVSGRSVQELHYTKELGEEAAYTSQMLIOTAR 120

DB 61 LGLLAFGALALGLRMAIETNLEQLWVEVSGRSVQELHYTKELGEEAAYTSQMLIOTAR 120

QY 121 QRGENTLTPEALGLHLQALTASKVOVSLYKSWDLNKICYKSGVPLIENGMIEMIEKL 180

DB 121 QRGENTLTPEALGLHLQALTASKVOVSLYKSWDLNKICYKSGVPLIENGMIEMIEKL 180

QY 181 FFCVILTPDLCFWEKAGKQGSAYLPGRPDIQWNTNLDPEQLLEELGPPFASLGGFRELDDK 240

DB 181 FFCVILTPDLCFWEKAGKQGSAYLPGRPDIQWNTNLDPEQLLEELGPPFASLGGFRELDDK 240

QY 241 AQVGQAYVGRPCILHPDDDLHCPSPAPNHHSHRQAPNVAHELGGCHGFSGHFMHQEBLLG 300

DB 241 AQVGQAYVGRPCILHPDDDLHCPSPAPNHHSHRQAPNVAHELGGCHGFSGHFMHQEBLLG 300

QY 301 GWARDPOQELLRAEALQSTELFMSPROLYEHPRGDYQTHDTCWSEQASTVLQAWQRREV 360

DB 301 GWARDPOQELLRAEALQSTELFMSPROLYEHPRGDYQTHDTCWSEQASTVLQAWQRREV 360

QY 361 QLAQALPENASQIHAFFSTTLDLILHAFSEVSARVVGYYLLMALVACVTMLRWDCAQ 420

DB 361 QLAQALPENASQIHAFFSTTLDLILHAFSEVSARVVGYYLLMALVACVTMLRWDCAQ 420

QY 421 SQGSVGLAGVILVALAVASGLGCLCALLGITFNAATTQVLPFLALGIGVDDVELLAHAFTE 480

DB 421 SQGSVGLAGVILVALAVASGLGCLCALLGITFNAATTQVLPFLALGIGVDDVELLAHAFTE 480

QY 481 ALPGTFLQRMGECLORTGTSVLTSLNNMAFLMAALVPALRAFSLQAAIVVGCCTFV 540

DB 481 ALPGTFLQRMGECLORTGTSVLTSLNNMAFLMAALVPALRAFSLQAAIVVGCCTFV 540

QY 541 AVMLVFPAILSLDRLRRHRCQRLDVLCCFSSPCSAQVQIILPQELGDTGTVPGIAHLTATV 600

DB 541 AVMLVFPAILSLDRLRRHRCQRLDVLCCFSSPCSAQVQIILPQELGDTGTVPGIAHLTATV 600

QY 601 QAFTHCEASSQHVVTILPPQAHVLPSPDPLGSELFPSPGSTRDLGQEEETROKAAACKS 660

DB 601 QAFTHCEASSQHVVTILPPQAHVLPSPDPLGSELFPSPGSTRDLGQEEETROKAAACKS 660

QY 661 LPCARWNLAHFARYOFAPLLQSHAKAIVLFGALLGLSLYGATLVQDGLALTDVVRPG 720

DB 661 LPCARWNLAHFARYOFAPLLQSHAKAIVLFGALLGLSLYGATLVQDGLALTDVVRPG 720

QY 721 TKEHAFSLAQURYFSLYSEVALVTGGFDYAHSQBALFDLHORFSSSLKAVLPPPTQAPRT 780

DB 721 TKEHAFSLAQURYFSLYSEVALVTGGFDYAHSQBALFDLHORFSSSLKAVLPPPTQAPRT 780

QY 781 WLHYRNWLOGIQAAFQDQWASGRITRHSYRNGSEGDGALAYKLLIQTGDAQEPLDFSOLT 840

DB 781 WLHYRNWLOGIQAAFQDQWASGRITRHSYRNGSEGDGALAYKLLIQTGDAQEPLDFSOLT 840

QY 841 TRKLVDREGLIPPELFYMWGLTVMVSSDPLGLAASQAFYPPPPWHLHDKYDTTGENLRIP 900

DB 841 TRKLVDREGLIPPELFYMWGLTVMVSSDPLGLAASQAFYPPPPWHLHDKYDTTGENLRIP 900

841 TRKLVDRGLIPPELFYMGCLTVWVSSDPLGLAASQANFYPPPEMLHDKYDTTGENLRIP 900
901 PAQPLEFAQFPPLRLGLQKTADFVAIEGARAACAEAGQAGVHAYPSGPFLEWQYLG 960
901 PAQPLEFAQFPPLRLGLQKTADFVAIEGARAACAEAGQAGVHAYPSGPFLEWQYLG 960
961 RECFLLAVCILLVCTFLVCAALLNPWTAGLIVLVMVTVLFGIMGLGKLSAIPV 1020
961 RECFLLAVCILLVCTFLVCAALLNPWTAGLIVLVMVTVLFGIMGLGKLSAIPV 1020
1021 ILVASGIGVEFTVHVALGFLTTQGSRLNRAAHLEHTFAPVTDGAISTLLGLMAGSH 1080
1021 ILVASGIGVEFTVHVALGFLTTQGSRLNRAAHLEHTFAPVTDGAISTLLGLMAGSH 1080
1081 FDFIVRYFAALTUTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPPAPQGG 1140
1081 FDFIVRYFAALTUTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPPAPQGG 1140
1141 LRWASSSLUQSFARVTTSMVTAIHPPPLPGAYIHPADPEPPWSPATSSGNLSRGPGP 1200
1141 LRWASSSLUQSFARVTTSMVTAIHPPPLPGAYIHPADPEPPWSPATSSGNLSRGPGP 1200
1201 ATG 1203
1201 ATG 1203
RESULT 5
ID AAY92703 standard; protein; 1203 AA.
XX AAY92703;
AC AAY92703;
XX AAY92703;
DT 10-AUG-2000 (first entry)
DE Human patched 2 (PTCH2) protein splice variant.
DE Patched 2; PTCH2; 1p32-35; tumour suppressor; familial melanoma CMML;
KW familial adenomatous polyposis; hMcm1; Michelin Tire Baby Syndrome;
KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
KW basal cell carcinoma; gene therapy; chromosome 1p32-35; splice variant.
XX Homo sapiens.
XX WO200020037-A1.
XX 13-APR-2000.
XX 06-OCT-1999; 99WO-SE001784.
XX 06-OCT-1998; 98SE-00003393.
XX (KARO-) KAROLINSKA INNOVATIONS AB.
PA (PHAA) PHARMACIA & UPJOHN CO.
XX Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
PI Hollingsworth RE;
XX WPI; 2000-303645/26.
DR N-PSDB; AAA09084.
XX Isolated human protein capable of participating in human patched
PT gene/Sonic hedgehog pathway during embryonic development is used in
PT medicament for treatment of condition involving tumors such as basal cell
PT carcinoma.
XX Disclosure; Page; 55pp; English.
XX This protein is a splice variant encoded by the novel human patched 2
CC gene (PTCH2), which has been localised by radiation hybrid mapping to
CC chromosome 1p32-35 with DIS211 and W1404 as closest flanking markers and
CC with an estimated localisation 5.5 cR from DIS443. This region is often
CC lost by LOH in various different tumour types, such as neuroblastoma,

CC melanoma and breast and colon cancer. PTCH2 is a candidate for a tumour
CC suppressor gene in this region. It is also a candidate gene for
CC involvement in familial melanoma CMML, modifier locus for familial
CC adenomatous polyposis hMcm1 and Michelin Tire Baby Syndrome. PTCH2 is
CC capable of participating in the human patched gene/Sonic hedgehog
CC (PTCH/SHH) pathway during embryonic development and/or carcinogenesis.
CC The isolated human protein is useful as a medicament for the treatment of
CC a condition involving tumours such as BCC (basal cell carcinoma). The
CC nucleic acid is useful in gene therapy, and for use as a probe, primer or
CC a diagnostic agent. Note: this sequence was constructed using information
CC from Figure 2B and the protein sequence given on pages 41-44 of the
CC specification
XX Sequence 1203 AA;
SQ
Query Match 99.5%; Score 6238; DB 3; Length 1203;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1199; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MTRSPPLRELPSYTPPARTAAPQILAGSLKAPLMLRAYFQGLLFSLGGCIQRHCGKVL 60
DB 1 MTRSPPLRELPSYTPPARTAAPQILAGSLKAPLMLRAYFQGLLFSLGGCIQRHCGKVL 60
QY 61 LGLAFGALALGLRMAIITETNLEQLWVEGSRVSOELHYTKELGEEAAYTSQMLTQTAR 120
DB 61 LGLAFGALALGLRMAIITETNLEQLWVEGSRVSOELHYTKELGEEAAYTSQMLTQTAR 120
QY 121 QEGENILTPREALGLHQAALTASKQVVSILYKSWDLNKICYKSGVPLIENGMIEMIEKL 180
DB 121 QEGENILTPREALGLHQAALTASKQVVSILYKSWDLNKICYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPLDCFEWGAQKQGSAYILPGRPDIQWNTLDPQLLEELGFFSLGFEFLDLK 240
DB 181 FPCVILTPLDCFEWGAQKQGSAYILPGRPDIQWNTLDPQLLEELGFFSLGFEFLDLK 240
QY 241 AQVQAYVGRPCILHPDDLHCPSPAPNHHSRQAPNVAHELSCGCHGSHKFMWQEBLLG 300
DB 241 AQVQAYVGRPCILHPDDLHCPSPAPNHHSRQAPNVAHELSCGCHGSHKFMWQEBLLG 300
QY 301 GMDPQGBLLRAEALQSTFLLMSPRQLYHEHGRDYQTHDIGWSEQAQSTVLQAWORRFV 360
DB 301 GMDPQGBLLRAEALQSTFLLMSPRQLYHEHGRDYQTHDIGWSEQAQSTVLQAWORRFV 360
QY 361 QLAQZALPENASQOIHAFSSTLLDDILHAFSEVSARVVGYYLLMAYACVTLRWDCAQ 420
DB 361 QLAQZALPENASQOIHAFSSTLLDDILHAFSEVSARVVGYYLLMAYACVTLRWDCAQ 420
QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDVDFLLAHAFTE 480
DB 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDVDFLLAHAFTE 480
QY 481 ALPGTQLQRMGECLOQTGTSVVLTSINNMAAFMAALVPIPALRAFSQAALVVGCTFV 540
DB 481 ALPGTQLQRMGECLOQTGTSVVLTSINNMAAFMAALVPIPALRAFSQAALVVGCTFV 540
QY 541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVIQILPQELGDTGTPVPGIAHLTATV 600
DB 541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVIQILPQELGDTGTPVPGIAHLTATV 600
QY 601 QAPTHCEASSQHVVTILPQOAHLVPPSPDLGSELSPGSGSTRDLIGQEBEETKQKAACKS 660
DB 601 QAPTHCEASSQHVVTILPQOAHLVPPSPDLGSELSPGSGSTRDLIGQEBEETKQKAACKS 660
QY 661 LPCARNWLAHFARYQAPLILLOSHAKAIVLVPFALLGLSLYCATLVQDGLAITDVVPRG 720
DB 661 LPCARNWLAHFARYQAPLILLOSHAKAIVLVPFALLGLSLYCATLVQDGLAITDVVPRG 720
QY 721 TKEHAFSLAQRLYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSSLKAVLPPPATQAPRT 780
DB 721 TKEHAFSLAQRLYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSSLKAVLPPPATQAPRT 780
QY 781 WLHYRNWLGIOQAADFQDQWASGRITRHSYRNCSEDEGALAYKLLIQTGDAQEPDLFSQLT 840

Db 781 WLHYRNWLQGIQAAPDQDQWASGRITRHSYRNGSEGDALAYKLLIQTQDAQLLDFSQLT 840
 QY 841 TRKLVDRGLIPPELFYMGLTWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
 Db 841 TRKLVDRGLIPPELFYMGLTWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
 QY 901 PAQPLEFAQFPFLRLGLQKTADFVEAIEGARACACAEAGQAGVHAYPSGSPFLFWEQYGLG 960
 Db 901 PAQPLEFAQFPFLRLGLQKTADFVEAIEGARACACAEAGQAGVHAYPSGSPFLFWEQYGLG 960
 QY 961 RRCFLAVCILVCTFLVCAALLLNPWTAGLIVLVLAMTVLFGIMGLIKLSAIPVY 1020
 Db 961 RRCFLAVCILVCTFLVCAALLLNPWTAGLIVLVLAMTVLFGIMGLIKLSAIPVY 1020
 QY 1021 ILVASGVIGVEFTVHALGFLTQGSRLRAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
 Db 1021 ILVASGVIGVEFTVHALGFLTQGSRLRAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
 QY 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPPAQGGG 1140
 Db 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPPAQGGG 1140
 QY 1141 LRWGASSLPQSFAVTTSMTVAIHPPPLPGAYIHPADPEPWSPAATSSGNLSSRGPGP 1200
 Db 1141 LRWGASSLPQSFAVTTSMTVAIHPPPLPGAYIHPADPEPWSPAATSSGNLSSRGPGP 1200
 QY 1201 ATG 1203
 Db 1201 ATG 1203

RESULT 6

AA92225
 ID AA92225 standard; protein; 1146 AA.
 AC AA92225;
 XX
 DT 10-AUG-2000 (first entry)
 DE Human patched 2 (PTCH2) protein.
 XX
 KW Patched 2; PTCH2; tumour suppressor; familial melanoma CMM1;
 KW familial adenomatous polyposis; hMomi; Michelin Tire Baby Syndrome;
 KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
 KW basal cell carcinoma; chromosome 1p32-35; gene therapy.
 OS Homo sapiens.
 FN WO200020037-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 06-OCT-1999; 99WO-SE001784.
 XX
 PR 06-OCT-1998; 98SE-00003393.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Zaphiropoulos FG, Unden AB, Toftgard R, Rahnama F;
 PI Hollingsworth RE;
 XX
 DR WPI; 2000-303645/26.
 DR N-FSDB; AAA09081, AAA09084.
 XX
 PT Isolated human protein capable of participating in human patched
 PT gene/sonic hedgehog pathway during embryonic development is used in
 PT medicament for treatment of condition involving tumors such as basal cell
 PT carcinoma.
 XX
 PS Claim 2; Page 41-44; 55pp; English.
 XX
 CC This protein is encoded by the novel human patched 2 gene (PTCH2), which

CC has been localised by radiation hybrid mapping to chromosome 1p32-35 with
 CC DIS11 and W1404 as closest flanking markers and with an estimated
 CC localisation 5.5 cR from DIS443. This region is often lost by LOH in
 CC various different tumour types, such as neuroblastoma, melanoma and
 CC breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
 CC gene in this region. It is also a candidate gene for involvement in
 CC familial melanoma CMM1, modifier locus for familial adenomatous polyposis
 CC hMomi and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene
 CC exist (see AAA09082-84). PTCH2 is capable of participating in the human
 CC patched gene/sonic hedgehog (PTCH/SHH) pathway during embryonic
 CC development and/or carcinogenesis. The isolated human protein is useful
 CC as a medicament for the treatment of a condition involving tumours such
 CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
 CC therapy, and for use as a probe, primer or a diagnostic agent

XX Sequence 1146 AA;

Query Match 94.2%; Score 5911; DB 3; Length 1146;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1139; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLMLRAYFQGLLFSGLGGIORHCGKVL 60
 Db 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLMLRAYFQGLLFSGLGGIORHCGKVL 60
 QY 61 LGLAFGALALGLRMAIETNLEQWVEVGSVSOELHYTKEKLGEEAAYTSQMLIQAT 120
 Db 61 LGLAFGALALGLRMAIETNLEQWVEVGSVSOELHYTKEKLGEEAAYTSQMLIQAT 120
 QY 121 QEGENILTPREALGLHLQAALTASKVQVSLYKSWDLNKKCYKSGVPLTENGMIEMIEKL 180
 Db 121 QEGENILTPREALGLHLQAALTASKVQVSLYKSWDLNKKCYKSGVPLTENGMIEMIEKL 180
 QY 181 FPCVILTPDCFWEGAKLQGSAYLPGRPDIQWNLDPQLEELGEPFASLEGFRELDDK 240
 Db 181 FPCVILTPDCFWEGAKLQGSAYLPGRPDIQWNLDPQLEELGEPFASLEGFRELDDK 240
 QY 241 AQVGQAYVGRPCPLHPDDLHCPSPAPNHHSRQAPNVAHELSCGCHGFSHKFWHQBELLG 300
 Db 241 AQVGQAYVGRPCPLHPDDLHCPSPAPNHHSRQAPNVAHELSCGCHGFSHKFWHQBELLG 300
 QY 301 GWARDPQGLARAFALQSTFLLMSPROLYEHRGDYQTHDIGNSEBQASTVLOAWQRRFV 360
 Db 301 GWARDPQGLARAFALQSTFLLMSPROLYEHRGDYQTHDIGNSEBQASTVLOAWQRRFV 360
 QY 361 QLAQELPENASQOIHAFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
 Db 361 QLAQELPENASQOIHAFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
 QY 421 SQGSVGLAGVLLVALAVASGLGALLGITNAATTQVLPFALIGVDVFLLAHAFTE 480
 Db 421 SQGSVGLAGVLLVALAVASGLGALLGITNAATTQVLPFALIGVDVFLLAHAFTE 480
 QY 481 ALPGTPIQERMGECLQRTGTSVLTSTNNMAAFMLAALVPIPALRAFSLQAAIVVGCTFV 540
 Db 481 ALPGTPIQERMGECLQRTGTSVLTSTNNMAAFMLAALVPIPALRAFSLQAAIVVGCTFV 540
 QY 541 AVMLVFPAILSLDLRRRHCRQLDVLCCFSSPCSAQVIQILPQELGDGVTPVGIHLTATV 600
 Db 541 AVMLVFPAILSLDLRRRHCRQLDVLCCFSSPCSAQVIQILPQELGDGVTPVGIHLTATV 600
 QY 601 QAFTHCEASSQHVVTILPPQAHLVPPSPDPLGSELSFPGSSTRDLLGQEEETROKAAACKS 660
 Db 601 QAFTHCEASSQHVVTILPPQAHLVPPSPDPLGSELSFPGSSTRDLLGQEEETROKAAACKS 660
 QY 661 LPCARWNLAHFARYQFAPLILQSHAKAIVLVFQALLGLSLYATLVQDGLALTDVVPRG 720
 Db 661 LPCARWNLAHFARYQFAPLILQSHAKAIVLVFQALLGLSLYATLVQDGLALTDVVPRG 720
 QY 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSLKAVLPPPTQAPRT 780
 Db 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSLKAVLPPPTQAPRT 780

Qy	1140 G	1140
Db	1248	1307

Qy	1141	-----LWVG-----	-----ASSLPGQFAR	1155
Db	1308	REGLWPLYPRRDFAETSTEGHSGPSNRARPGARSHNPRNPASTAMGSSVEGYCQP		1367
Qy	1156	VTT-----SMTVAIHPPPLFCAYIHP	1176	
Db	1368	ITTVTASGASVTVAVHPDPVFPQPGNPF	1393	

RESULT 9	
AAW52200	AAW52200 standard; protein; 1447 AA.
XX	
XX	AAW52200;
XX	
XX	25-JUN-1998 (first entry)
DT	
XX	
XX	Human patched (ptc) protein.
DE	
XX	
XX	Patched protein; ptc; cancer; tumour suppressor; cell adhesion promoter;
KW	wound healing; ageing; human.
KW	
XX	
OS	Homo sapiens.
OS	
XX	
XX	W09745541-A2.
XX	
PD	04-DEC-1997.
XX	
XX	02-JUN-1997; 97WO-US009553.
XX	
XX	31-MAY-1996; 96US-00656055.
PR	
XX	
XX	(STRD) UNIV LELAND STANFORD JUNIOR.
FA	(REGC) UNIV CALIFORNIA.
FA	
XX	
XX	Scott MP, Goodrich LV, Johnson RL, Epstein E, Oro A;
PI	
XX	
XX	WPI: 1998-032648/03.
DR	N-PSDB; AAV21590.
DR	
XX	
XX	
PT	Patched protein other than Drosophila melanogaster patched protein - used
PT	for characterising the phenotype of a tumour.
PS	
PS	Claim 4; Page 76-80; 86pp; English.

This is a human patched (ptc) protein. The encoding DNA can be used to construct an expression cassette comprising an altered patch or hedgehog gene. The expression cassette comprises a nucleic acid encoding a patched protein other than a *Drosophila melanogaster* patched protein, or fragment of at least 12 nucleotides in length, as other than an intact chromosome, under transcriptional control of a transcriptional initiation region, and, a transcriptional termination region, both functional in an expression host. A genetically engineered mammalian cell comprising this expression cassette as an extrachromosomal element or integrated into the genome of the cell can be predisposed to develop basal cell carcinoma as a result of the transfection. By analysing DNA, functional analysis of patched protein function, or by detecting antibody binding to abnormal patched protein, a genetic predisposition to developmental abnormalities and cancer can be diagnosed. This analysis can also be used for characterising the phenotype of a tumour, particularly a carcinoma, especially a basal cell carcinoma. The methods can also be used for characterising transitional cell carcinoma of the bladder, meningiomas and medulloblastomas, etc. The modified cells comprising the expression cassette can be used to determine the role of different exons of the patched gene in oncogenesis, signal transduction, etc. Transgenic animal models created from these cells can be used as animal models for carcinomas of the skin. The patched protein of mosquito, butterfly or beetle or alternatively, a mammalian patched protein of human or mouse

CC can be used to identify ligands or substrates that bind to, modulate, or
CC mimic the action of patched gene. These agents could be used as tumour
CC suppressors, cell adhesion promoters (e.g. in wound healing and ageing)
XX
SO Sequence 1447 AA;

Query Match.	53.4%;	Score 3348;	DB 2;	Length 1447;
Best Local Similarity	49.9%;	Pred. No. 1.5e-291;		
Matches	672;	Conservative 203;	Mismatches 285;	Indels 186; Gaps 18;
Qy	12	PSYTPPARTAAPQILAGSL--KAPLWLRAVFQGLLFSLGCGIQRHCGKVLFLGLLAFGA	68	
Db	53	PSYC-DAAFLEQISGKGATGRKAPLWLRKAFORLLFKLGCYIQKCGKFLVVGLLIFGA	111	
Qy	69	LALGLRMAIITETNLEQLWVEGSRVSQELHYTKEKLGEEAAYTSQMLIQIQTARQEGENILT	128	
Db	112	FAVGLKAANLETNVEELWVEGGRVSRELNYTRQKIGEEAMFNQPMIQITPKEEGANVLT	171	
Qy	129	PEALGHILQAAITASKKVQNSLYGKSDNLNKICVKSGVPLIENGMIEMWIEKLPPCVILTP	198	
Db	172	TEALLQHLDSALQASRVHVYMYNRQMKLEHLCYKSGELITETGYMPOIIBYLPCJLIITP	231	
Qy	189	LDFCWEGAKLQGSAYLPGRPDIQTWNLDPEQLLEELGPF-ASLEGFRELLDKAQQVOAY	247	
Db	232	LDFCWEGAKLQSGTAYILLGXPLRWTFNDFLEFLEELKKNYQVDSWEEMLNKAENVGHY	291	
Qy	248	VGRPCILHPDDLCPSPAPNHHRSQAPNVAHELGGCGHGFHKPMHWQEEILLGGMARDPQ	307	
Db	292	MDRPCLNPADPDPCFATAPNKNSTKPLDMALVINGGCHGSLRKYMHVQEEILVIGTVKNST	351	
Qy	308	GELLRAEALQSTFLLMSPROLYEHPRG-DYQTHDIGWSEEQASTVLQAWORRVQLAAQEA	366	
Db	352	GKLVSALHQTQMLTPKMYHFHGYEVSH-INNNEDKAAAILAEAWORTYVEVVHQ	410	
Qy	367	LPENASQOIHAFSGSTLDDTLHAFSEVSARVVGYYLLMLAYACTVMLRWDCAQSGSVG	426	
Db	411	VAONSTQKVLSPFTTLLDDILKSFSDSVIRVASGYLLMLAYACTVMLRWDCKSQGAVG	470	
Qy	427	LAVLLVALAVASGLGLCALLGTTFNAATQVLPFLALGIVDDVDFLLAHAFTEALPG--	484	
Db	471	LAVLLVALSVAAGLGLCSLIGISFNAATQVLPFLALGVDDVDVFLAHAFSETGONKR	530	
Qy	485	TPQERMEGCLQRTGTSVWLTSINNNAAFLMAALVPIPALRAFSLQAAIVVGCTEFAVML	544	
Db	531	IPEDRTGECCKRTGASVALTSISNVAFFMAALIPALRAFSLQAAVVVVVNFAMVLL	590	
Qy	545	VFPAILSLDURRHRCORLDVLCFSPSCSAQVITQLPQELGD-----GTVPVGTIAH--	595	
Db	591	IFPAILSMDLYRREDRLDFCCFTSPCVSRVLIQVEPQAYTDTHDNTRYSPPPYSSHSF	650	
Qy	596	-----LTATVQAFTHCEASSOHVVTILPQAHLVPPP-----SDPLGSELFPGGSTRD	644	
Db	651	AHETQITMQSTVQLRTEYDPHTHYVYTTAPRSEISVQPVTVTQDTLSCQSPSESTSTRD	710	
Qy	645	LLGQEBETRQKAACKSLPCARWNLAHFARYQAPAPLLIQSHAKAIVLVFLGALLGLSLYGA	704	
Db	711	LLSQFSDS--SLHCLBPPCTKWTLSSEFAEKHYAPFLKPKAKVVVILFLGLLGVLSLYGT	768	
Qy	705	TLVQDGLALTVPVPGRTKEHAFLSAQRYFSLYEVALVTQGGDFYAHSORALFDLHQRES	764	
Db	769	TRVRQGLDLTDIVPRETREYDFIAAQFKYFSPFYNMVIVTQKA-DYPNIQHLLYDLHRSFS	827	
Qy	765	SLXAVLPPPTAQAPRTWLHYRYRWLQGIQAAPQDQWASGRI TRHSYRNGSEDCALAYKLL	824	
Db	828	NVXYVMLEENKQLEPKMWLHYFRDQWLQLODAFSDDWETGKIMPNPNYKNGSDDDGLAYKLL	887	
Qy	825	IQTGDAQEPDLDFSQLTRKLVDRREGILPPLELFYMGLTIVVWSSDPLGLAASQANFYPPPE	884	
Db	888	VQTGSRDKPIDIQLTKQRLVDADGILNSAFYIYLTAWSNNDPVAYASQANIRPHRPE	947	
Qy	885	WLHDKDYDTTGE-NLRITPPAQPLFAQFPFLRLGLQKQTADFVEALLEGARAAACAGAQGVH	943	
Db	948	VWHDKADYMPETRLRIPAAEPYEAQFPFYNLGRJRTSDFEATEKVRTTICSNYTSIGLS	1007	


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QY 765 SLKAVLPPEPATOAPTWTWLYHYNWLOGIOAAFDQDNASGRITRHSYRNGSDGALAYKLL 824
Db 828 NVKYVWLEENKQPKWMLHYFRDQLQLOAFDSWETGKIMPNYKNGSDGVLAYKLL 887
QY 825 IQTDAQEPLDFSLTRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPE 884
Db 888 VOTGSRDKPIDISQLTKQRLVDADGIINPSAFIYILTAWVNDPVAYASQANIRPHE 947
QY 885 WLHDKYDTTGE-NLRTPPAQPIEFAPFPFLRLGQKTADFVEAIEGARACACAGAGYH 943
Db 948 WHDKADYMPETRLRIPAAEPIEYAFQFPFLNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007
QY 944 AYEGSGPELFWEQYGLRRCFLFLLAVCTFLVCALLILNPWTAGLVLVLAMTVEL 1003
Db 1008 SYENGYPFLFWEQYIGLRHWLLFISVLIACFLVCALLNPWTAGIIVMLAMTVEL 1067
QY 1004 FGIMFGLIKLSAIPVILVASVIGIVETVHVVALGFLTTQGSRLNRAAAHLEHTFAPVT 1063
Db 1068 FGMWGLIGIKLSAIPVILVASVIGIVETVHVVALAFLTAIGDKNRAVALAHEMFAPVL 1127
QY 1064 DGAISTLLGLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPIV-- 1121
Db 1128 DGAISTLLGLVLMAGSEFDFIVRYFFAVALAILTLGLVNLGLVLLPVLLSFFGYPPEVSPA 1187
QY 1122 ----QWYKESPE-----ILSPP-----APQGG 1139
Db 1188 NGLNRLPTSPFPFPSPVVRFPMPGGTHSGSDSDSEYSSQTTVSGLSBELRHYEAQQA 1247
QY 1140 G-----LRWG-----ASSLPOSFAR 1155
Db 1248 GGPAPHQVIVEATENPVFAHSTVVPBESRHHPPSPNPQQPHLDGSLPPGRCQQQPRDRPP 1307
QY 1141 -----LRWG-----ASSLPOSFAR 1155
Db 1308 REGMLPYRPRDAFEISTEGHSGFSNRARWGPARGSHNPNRNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAVIHP 1176
Db 1368 IITVTASAVTVAVHPPPPVPGGRNP 1393

RESULT 12
AAEI9830
ID AAEI9830 standard; protein; 1447 AA.
AC AAEI9830;
XX
XX
XX 18-JUN-2002 (first entry)
XX Human patched (Ptch) protein.
XX Human; patched; Ptch; cell proliferation; differentiation; therapy;
XX cytostatic; testicular cancer; hedgehog protein signalling.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 100..119
XX /label= TM1
XX /note= "Transmembrane domain"
XX Domain 438..458
XX /label= TM2
XX /note= "Transmembrane domain"
XX Domain 471..493
XX /label= TM3
XX /note= "Transmembrane domain"
XX Domain 502..521
XX /label= TM4
XX /note= "Transmembrane domain"
XX Domain 548..570
XX /label= TM5
XX /note= "Transmembrane domain"

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FT Domain 578..599
FT /label= TM6
FT /note= "Transmembrane domain"
FT Domain 751..769
FT /label= TM7
FT /note= "Transmembrane domain"
FT Domain 1028..1048
FT /label= TM8
FT /note= "Transmembrane domain"
FT Domain 1052..1074
FT /label= TM9
FT /note= "Transmembrane domain"
FT Domain 1078..1097
FT /label= TM10
FT /note= "Transmembrane domain"
FT Domain 1122..1141
FT /label= TM11
FT /note= "Transmembrane domain"
FT Domain 1155..1178
FT /label= TM12
FT /note= "Transmembrane domain"
XX US6348575-B1.
XX 19-FEB-2002.
XX 15-APR-1999; 99US-00293505.
XX 15-APR-1998; 98US-0081884P.
XX (GETH ) GENENTECH INC.
XX De Sauvage F, Carpenter DA;
XX WPI; 2002-215260/27.
XX Native human patched-2 polypeptide for treating disorders caused by
XX Hedgehog protein signaling such as testicular cancer, and for screening
XX cDNA libraries.
XX Example 1; Fig 3; 82pp; English.
XX The invention relates to an isolated sequence comprising a native human
XX patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
XX and mediator molecules in the hedgehog (Hh) cascade which are involved in
XX cell proliferation and differentiation. The isolated sequence is useful
XX for the treatment of disorders which are linked to Hedgehog, especially
XX Desert hedgehog expression, such as testicular cancer. It may also be
XX used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
XX homologues, and to diagnose whether a disorder is driven by Ptch-2 or
XX Hedgehog protein signalling. The present sequence is human patched (Ptch)
XX protein. Note: The sequence shown as SEQ ID NO: 4 in sequence listing of
XX the specification is a fragment of the sequence shown as SEQ ID NO: 4 in
XX fig 3 of the specification
XX
XX Query Match 53.4%; Score 3348; DB 5; Length 1447;
XX Best Local Similarity 49.9%; Pred. No. 1.5e-291;
XX Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
QY 12 PSYTPPARTAAPQILAGSL---KAPLMRAYFQGLLPSLGGCIQRHCKVFLGLLAFGA 68
Db 53 PSYC-DAFALEQISKGKATGRKAPLWLRKAFQRLLPKLGCVIQKCGKFLVWGLLIFGA 111
QY 69 LALGLRMAIETNLEQLWVEVGSVQELHYTKELGEEAAYTSOMLIQTARQGENILT 128
Db 112 FAVGLKAANLETNVEELWVEVGGVRSRELYTRQKIGEEAFNPQIMTQTPKEGANVLT 171
QY 129 PEALGLHLQAALTASKVQVSLYKGSWDLNKLTCYKSGVPLIENGMEIWKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHVYVYNRQWKLHLCYKSGELITETGYWDQIIEYLYPCLLIPT 231

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[illegible]

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Qy 129 PEALGHLQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMEIWMTEKFLPPCVILTP 188
Db 172 TEALCHLDSALQAQRVHVYMYNRQWKLHLCYKSGELITETGYMDQIIIEYLYPCLIIPT 231
Qy 189 LDCFWEGAKLQGSAYLPGRPDIQWNLDPOLLELPGPF-ASLEGFRELIDKAQVGOAY 247
Db 232 LDCFWEGAKLQSGTAYLGLKPLRTNTPDFLELBEKKINYQVDSWEMLNKAIEVGHGY 291
Qy 248 VGRPCILHDDHCPSPAPNHHSRQAPNAHVELSGGCHGFSHKFMHQEELLGGMARDPQ 307
Db 292 MDRPCINPADPCPATAPNKNSTKPLDMALVNGGCHGLSRKYMHWQEBELIVGVTVKST 351
Qy 308 GELLRAEALOSTFLILMSPLQYEHFRG-DYQTHDIGNSEEQASTVLQAWQRFPVOLAQBA 366
Db 352 GKLVSAAHALQTNFQMTPKQMYEHFKGYEVSH-INWNEDKAAALEAMQRTYVEVHQS 410
Qy 367 LPENASQOIHAFTSTLDDILHAFSEVSAARVVGVLMLAYACVTMLRWDCQAQSGSVG 426
Db 411 VAQNSTQKVLSTFTITLDDILKFSFSDSVIRVASGYLLMLAYACLMLRWDCSKSQGAVG 470
Qy 427 LAGVLLAVASGLGLCALLGITNAATQVLPFLALGIGVDVDFLLAHAFTEALPG-- 484
Db 471 LAGVLLVALSVAAGLGLCSLIGISFNAATQVLPFLALGVGVDVDFLLAHAFSETQNKR 530
Qy 485 TPLQRMGECLORTGTSVVLTSINNMAFLMAALVPIPALRAFSLOAIVUGCTFVAVML 544
Db 531 IPFEDTGECLKRTGASVALTSISNVTAFPMALIPALRAFSLOAAVVVVFNAFVLL 590
Qy 545 VFPAILSLDLRRHRCORLDVLCFSPCSAQAQVILPOELGP-----GTVPVGIAH-- 595
Db 591 IFPAILSMDLRYRDERLDIFCCFISPCVSRVQVPEQAYDTHNTRYSPPPPSSHSF 650
Qy 596 -----LTATVQAFTHCEASSQHVVTILPPOAHLVPPP-----SDPLGSELSFGGSTRD 644
Db 651 AHEQTQITWQSTVQLRTEDPHVHYTTAEPSEISVQPVTVTQDTLSCQSPESSTSD 710
Qy 645 LLGQEEETROKAAKSLCARWNLAHFARYQAPLILLOSHAKAIVLVLFGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPECTKWLTSFSAEKHYAPFLPKARVVVIFLFLGLVLSYGT 768
Qy 705 TLVQDGLALTDPVPRGTKEHAFSLAQLRYSELYVALVTOGGFDYAHQSORALFDLHQRFS 764
Db 769 TRVRDGLDLDIVPRETRYDFIAAQFYFSYNNYIIVTOKA-DYPNIQHLDDYDHRFS 827
Qy 765 SLKAVLPPPATQAPRTWLHYRNWILQGIQAAPDQDWSGRITRHSYRNGSESGALAYKLL 824
Db 828 NVKYVMLEENKQPKWMLHYERDMLQGLQDAPFSDMETGKIMPNYKNGSDDGVLAYKLL 887
Qy 825 IOTGDAQEPLEFSQLTTRKLVDRGLIPPELFPYMGILTVMVSSDPLGLAASQANFYPPPPPE 884
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Qy 885 WLHDKYDTTGE-NLRIPPAQPLEPAQFPFLRLGLOKTADEVEATEGARAAAEACAAQAGVH 943
Db 948 WHDKADYMPETRLRIPAEIEYIAQFPFYNLGLRDTSDFVEAIEKVTICSNYTSLSGS 1007
Qy 944 AYPGSGPFLFEQYGLRRCFLAYCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVEL 1003
Db 1008 SYPNGYPFLFEQYIGLRHLLLFISVVLACTFLVCVFLNPNWTAGIIVVVLAMMTVEL 1067
Qy 1004 FGIMFGLIGLSAIPVILVASVGVGVEFTVHVALGFLTTOGSRNLRAHALEHTFAPVT 1063
Db 1068 FGIMGLIGIGLSAIPVILVASVGVGVEFTVHVALGFLTTOGSRNLRAHALEHTFAPVT 1127
Qy 1064 DGAISTLLGLMLAGSHDFIVRYEFAALTVLTLGLLHGLVLLPVLVLSILGPPPEVI-- 1121
Db 1128 DGAISTLLGLMLAGSEDFIVRYEFAALTVLTLGLLHGLVLLPVLVLSILGPPPEVSPA 1187
Qy 1122 ---QMYKESPE-----ILSP-----APOGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRPAMPQGHTHSGSDSSDSEYSSQTTVSGLSLSEELRHYEAQQA 1247
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Qy 1140 G----- 1140
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Qy 1141 -----LRWG-----ASSLPOSFAR 1155
Db 1308 REGMLPPLYRPRRDAFEISTEGHSPSRARWPRGARSHNPNRPNASTAMGSSVPGYQCP 1367
Qy 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITTVTASAVTVAVHPPPVPGGRNP 1393

RESULT 14
AAG79571
ID AAG79571 standard; protein; 1447 AA.
XX AC AAG79571;
XX DT 23-DEC-2002 (first entry)
XX DE Human patched protein.
XX KW Patched; ptc; basal cell nevus syndrome; BCNS; wound healing;
KW developmental disorder; spina bifida; craniofacial abnormality;
KW basal cell carcinoma; skin; brain tumour; transgenic; mouse;
KW proliferation; oncogenesis; signal transduction; cancer; aging.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 113 /note= "Encoded by CCG"
FT Misc-difference 413 /note= "Encoded by GAG"
FT Misc-difference 864 /note= "Encoded by GAA"
XX US6429354-B1.
XX PD 06-AUG-2002.
XX PF 22-AUG-1997; 97US-00918658.
XX PR 07-OCT-1994; 94US-00319745.
XX PR 06-OCT-1995; 95US-00540406.
XX PR 31-MAY-1996; 96US-00656055.
XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Scott MP, Goodrich LV, Johnson RL, Epstein B;
XX DR WPI; 2002-722086/78.
XX DR N-FSDB; ABA00374.
XX PT Transgenic mouse, useful for cancer drug screening, comprises disruption
XX PT of allele of patched locus which predisposes the mouse to develop a
XX PT proliferative disorder.
XX PS Disclosure; Col 85-92; 58pp; English.
XX This sequence shows human patched (ptc) protein. Human patched gene has
XX been mapped to human chromosome band 9q22.3 and lies between two
XX polymorphic markers D9S196 and D9S287. Mutations in the patched gene are
XX characteristic in basal cell nevus syndrome (BCNS), an inherited disorder
XX with an increased risk of developmental disorders such as spina bifida
XX and craniofacial abnormalities, basal cell carcinoma of the skin and
XX brain tumours. The human and mouse ptc sequences show 86% homology. The
XX transgenic mouse of the invention has a genome comprising a disruption of
XX at least one allele of a patched locus, where the disruption predisposes
XX the mouse to develop a proliferative disorder. The transgenic mouse is
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CC useful for studying patched function and regulation, for e.g. a series of
CC small deletions and/or substitutions made in the patched gene, to
CC determine the role of different exons in oncogenesis, signal
CC transduction, etc; and for drug screening which is useful for treating
CC cancer or developmental abnormalities attributed to a defect in patched
CC function such as wound healing and aging
XX
SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 5; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
QY 12 PSYTPPAPTAQAQILAGSL--KAPLWRAVYQGLLFSIGCGIORHCGKVLFLGLAFA 68
DB 53 PSYC--DAAPALQISKGKATGRAPLWLRKAFQRLFLKLGICYIKCGKFLVVGLLIFGA 111
QY 69 LALGLRMALITNLEQLVEGSRVSQELHYTKELIGEBAAYTSQMLIQARQEGENILIT 128
DB 112 FAVGLKAANLEINVELWVEGVRSELNRYTRQKIGEBAEFPQLMIQTPEEGANVLT 171
QY 129 PFALGLHQAALITASKVQVSLYKGSWDLNKKIYKSGVPLIENGMIETWIEKLFPPCVILTP 188
DB 172 TEALLQLHLSALQASRVHYMYNRQWLEHLCYKSELITETGYMDQIIETLYPLCIITP 231
QY 189 LDCFEWAKLOGSAYLPCRPDIQNTNLDPEOLLELPGF--ASLEGFRELLDKAQQVQAY 247
DB 232 LDCFEWAKLOGSAYLPCRPDIQNTNLDPEOLLELPGF--ASLEGFRELLDKAQQVQAY 247
QY 248 VGRPCLLHPDRLCPSPAPNHHKQAPNVAHELSGGCHGFHFKFMHQWQELLGGMARDPQ 307
DB 292 MDRPCINPADPCPATAPKNKSTKPLDMALVNGGCHGLSRKYMHWQEBELIVGGTVKNT 351
QY 308 GELLRAEALQSTFLMSPQLYEHFRG--DYQTHDTGWSEEQASTVLQAWQRFLVLAQBA 366
DB 352 GLKVSAAHALQTMFQMLTPKQMYEHFKGYEVSH--INWNEDKAAALAEAWQRTYVEVHOS 410
QY 367 LPENASQOIHAFSTTLLDILHAFSEVSAARVGVYLLMAYACVTMLRWDCAQSGSVG 426
DB 411 VAQNSTQKVLSTTTTLLDILKSFSDSVIRVASGYLLMAYACVTMLRWDCKSQGAVG 470
QY 427 LAGVLLVALAVASGLCALGALGITRNAATQVLPFLALGIGVDVFLLAHAFTALPG-- 484
DB 471 LAGVLLVALSVAAGLGLCSLIGISFNAATQVLPFLALGVGVDVFLLAHAFSETGQNK 530
QY 485 TPLQRMGHCLORTGTSVVLTSINWMAFLMALVPIPALRAFSLOAAIVVCTFVAVWL 544
DB 531 IPFEDRTGECLEKRTGASVALTSISNVTAFPMALIPALRAFSLOAAIVVVFNFAMVLL 590
QY 545 VFPAILSLDLRRRHCRDLVLCFCSPSCSAQVITQILPQELGD-----GTPVVGIAH-- 595
DB 591 IFPAILSMDLRYREDRLDIFCCFTSPCVSRVIOVEPQAYTHTDNTRYSPPPYSSHSF 650
QY 596 -----ITATVQAFTHCBASSQHVVTILPQAHLVPPP-----SDPLGSELFSPGSTRD 644
DB 651 AHETQITMQSTVQLRTEYDPHTHYVYTTAEPRSEISVQPVTVTQDTLSCQSPSTSTRD 710
QY 645 LLGQEEETQKACAKSLPCARNWLAHFARYQFAPLLQSHAKAIVLVLPFALLGLSLYGA 704
DB 711 LLSQFSDS--SLHCLPEPPCTKWTLSFAEKHYAPFLPKARKVWIFLFLGLGVSLYGT 768
QY 705 TLVQDGLALTDDVPRGTKEHAFSLAQRYFSLYEVALVTQGGFDVAHSORALFDLHOFES 764
DB 769 TVRUGLDLTDIVPRETRYEDRIAQPKYFSFYNMYVITQKA--DYPNIQHLIYDLHRSFS 827
QY 765 SLKAVLPPPTAPQATRWLHYRNWLGIOAAFDQDQWASGRITRHAYRNGSEGCALAYKLL 824
DB 828 NVKYVMLENKQLPKQWMLHYFRDLWQLQDAFSDWQTKIMPNYKNGSDDDGLVAYKLL 887
QY 825 IOTGDAQEPLDPSLTTRKLVDEGLIPPELFVWGLTWVWSSDPLGLAASQANFYPPPE 884
DB 888 VQTGRDKDIDISQLTKQRLVADAGDGIINFSAFYIYLTAWVSNPDVAYAAASQANIRPHRE 947

QY 885 WLHDKYDTTGE--NLRIPPAQPLEFAQFPFLRLGLOKTDVFAIEGARACAEAGQGVH 943
DB 948 WHDKADADYWPETRLIRPAEPIEYQAQFFYLNGLRDTSDFEAIEKVRICSNYSLSLS 1007
QY 944 AYPGSPFLFWBQYIQLRRRCFLAYCILLVCTFLVCALLLNPWTAGLIVLVAMMTVEL 1003
DB 1008 SYNGPYPLFWBQYIQLRRHLLIFISVVLACTFLVCAVFLNPWTAGIIVVVLMTVEL 1067
QY 1004 FQIMGFLGILKLSAIPVILVASGVGVFVHVALGELTTCQSRNIRAAHALEHTFAPVT 1063
DB 1068 FQMGGLIGILKLSAVPWILIASVGVGVFVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127
QY 1064 DGAISTLLGLMLAGSHFDFIVRYFFAALTIVTLGLLHGLVLLFVLLSILGPPPEVI-- 1121
DB 1128 DGAISTLLGLMLAGSEDFIVRYFFAALVILITILGVNLGLVLLFVLLSFFGYPPEVSA 1187
QY 1122 ----QMYKESPE-----ILSP-----APQG 1139
DB 1188 NGLNRLPTSPPEPPSVVRFAMPGGTHSGSDSDSEYSSQTTVSGLSSELRYEAQQA 1247
QY 1140 G-----LRWG-----ASSSLPQSFA 1155
DB 1248 GGAHQVIVEATENPVFAHSTVVHPESRHHPPSNRQOPHLDSGLPPGRQOQRRDDPP 1307
QY 1141 -----LRWG-----ASSSLPQSFA 1155
DB 1308 REGLMPLRYRDRDAFEISTEGHSGPSNRWGPGRASHNPNPASTAMGSSVPGYCOP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
DB 1368 ITVTASASVTVAVHPPPVPGSGRNP 1393
RESULT 15
ABU62275
ID ABU62275 standard; protein; 1447 AA.
XX
AC ABU62275;
XX
DT 25-AUG-2003 (first entry)
XX
DE Human patched gene PTC product.
XX
KW Human; patched gene; PTC; hedgehog protein; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003032085-A1.
XX
PD 13-FEB-2003.
XX
PF 20-OCT-1997; 97US-00954701.
XX
PR 07-OCT-1994; 94US-00319745.
PR 06-OCT-1995; 95US-00540406.
XX
PA (SCOT/) SCOTT M P.
PA (GOOD/) GOODRICH L V.
PA (JOHN/) JOHNSON R L.
XX
PI Scott MP, Goodrich LV, Johnson RL;
XX
WPI; 2003-492065/46.
XX
PT New DNA sequence other than present in a chromosome encoding patched gene
PT other than Drosophila patched gene, useful for preparing transgenic
PT laboratory animals and to knock out patched protein in embryonic stem
PT cells.
XX
PS Disclosure; Page 8-10; 40pp; English.
XX
CC The invention relates to a DNA sequence other than present in chromosome
CC encoding a patched (ptc) gene other than Drosophila patched gene. A cell

expressing the DNA sequence is useful for producing patched protein, by growing the cell expressing the DNA sequence, where the patched protein is expressed and isolating the patched protein free of other proteins. The cell expressing the DNA sequence is also useful for screening candidate compounds for binding affinity to the patched protein, by combining the candidate protein with the cell expressing the DNA sequence where the DNA sequence comprises the entire coding sequence under the transcriptional regulation of the transcriptional initiation region and a transcriptional termination region functional in the cell, expressing the patched protein in the cell and assaying for the binding of the candidate compound to the patched protein. The above cell is useful for screening candidate compounds for agonist activity with the patched protein. The DNA sequence is useful for producing all or portions of the patched protein, as probes for research, diagnosis, binding of hedgehog protein for its isolation and purification and in gene therapy. The DNA sequence is also useful as primers for investigating other species and for isolating genes from various mammalian sources of interest, particularly from humans or from domestic animals. The DNA sequence is further useful for preparing transgenic laboratory animals and to knock out the PTC protein in the embryonic stem cells, so as to produce hosts with single functional patched gene. The present sequence represents the amino acid sequence of the human patched gene PTC product

Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 7; Length 1447;

Best Local Similarity 49.9%; Pred. No. 1.5e-291;

Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

12 PSYTPARTAAPOILAGSL---KAPLWRAVYFQGLLFLSGCIGIQHCGKVLFLGLLAFGA 68
 53 PSYC-DAAPALEQISKGATGKAPLWRAKFORLLFKLGVYQKNCGLVVGILLIFGA 111
 69 LALGLRMAIETNLQMLWVEGSRVSOBLHYTKELGSEAAVTSQMLIQTARQEGENILT 128
 112 FAVGLKAANLETNBELWVEGSRVSRLENYTRQKIGSEAMFNPQLMIQTPEEGANVLT 171
 129 PEALGLHQAALTASKVOVSLYKGSNDLKNICYKSGVPLIENGMEIWKELFPVCVILTP 188
 172 TEALQHLDSALQASRHHVYMYNRMQWKEHLCKYSGELITETGYMDQIIEYDPLCLIIPT 231
 189 LDCFWEGAKLOGGSAYLPCRPDIOWTNLDPEQLLELQPF-ASLRGFRLELDKAQVGOAY 247
 232 LDCFWEGAKLOGGTAYLLGKPLRWNTNFDPLFLBELKKINYQVDSWEEMLNKAEGHYG 291
 248 VGRPLCHPDDLHCPSPANHHSRQAPNVAAHLSGCGHFSKFMHQWQBELLLGGNWARDPQ 307
 292 MDRPLCNADPCPATAPNKSTKPLDMALVLNGGCHGLSRKRYMEHWQBELIIVGGTVKNST 351
 308 GELLRAEALQSTFLMSPROLYEHPRG-DYQTHDIGMSEEQASTVLOAWORRFVQLAQEA 366
 352 GKLVSAAHALQTMFQMTPKQMEHPKGEYVSH-INWNEDKAAALILEAWQRTYVEVHQ 410
 367 LPENASQOIHAFTSTLDDILHAFSEVSAARVVGGLYMLAYACVTMLRWDCASQSGSVG 426
 411 VAQNSTQKVLSPTTTLLDDLLKSFSDSVIRVASGYLLMAYACLTMLRWDCSKSQGAVG 470
 427 LAGVLLVALAVASGLGCLLIGITTNAAATTVLPFLALGIGVDDVFLLAHAFTALPG-- 484
 471 LAGVLLVALVAAAGLGLGSLGISFNAAATTVLPFLALGIGVDDVFLLAHAFTALPG-- 530
 485 TPLQRMGECLORTGTSVVLTSINNMAAFMLAALVPIPALRAFSLOAAIVVGCITVAVML 544
 531 IPFDRTGECUKRTGASVALTSISNVTAFMAALIPIPALRAFSLOAAIVVVFAMVLL 590
 545 VFPAILSLDLRRHRCORLDVLCFSSPCSAOVIQILPOELGD-----GTVPVGIAH-- 595
 591 IFFAILSMDLVREDRRLDIFCCFTSPCVSRVQIYEPQAYTDTHTNTRYSPPPPYSSHSF 650
 596 -----LTATVQAATHCEASSQHVVVTLIPPOAHLVPPP-----SDPLGSELFSPGGSTRD 644
 651 AHETQITWQSTVQLRTEYDPHTVYVYTTAEPRSEISVQPVTVTQDTLSCQSPESSTSD 710

QY 645 ILGQEEETQKAAKXSLPCARNLHAFAFYQFAPILLQSHAKAIYVLVFLGALLGLSLYGA 704
 DB 711 LLSQFSDS--SUHCLPEPCTKTWLSFAEKHVPFLPKAKVWVIFLFLGLLGVSLYGT 768
 QY 705 TLVQDGLALTVDVVRGTGTEHAFSLAQRLYFSLYEVALVTQGGFDYAHQSORALFDLHOREFS 764
 DB 769 FVRUGLDLTDIVPRETREYDFIAAQFYKFSYNNVYVITOKA-DYPTNIOHLLYDLHRSFS 827
 QY 765 SUKAVLPPTAQPTWHLHYRNWLGQIQAAFDQDQWASGRITRHSYRNGSEDEGALAYKLL 824
 DB 828 NVKYVMLEBNKQLPKWMLHYFRDMLQGLQDAFDSWETGKIMPNNYKNGSDGVLAYKLL 887
 QY 825 IOTGDAQEPDLDSOLTTRKLVDRGLIIPPELFYMGILTIVWSSDPIGLAASQANFPFPPPE 884
 DB 888 VQTGRDPEIDISQTKORLVADAGIINPSAFYIYLTAWVSNPDVAYASQANIRHPRE 947
 QY 885 WLHDKYDITGE-NLRIPPAQPLEFAQFPFLRLGLQKTADEFVAIEGARAACAEGAGVH 943
 DB 948 WYHDKADYMPETRLIPRAEPLEYAQFFPYLNGLDRTSDTFVEAIEKVRTICSNYTSLSLS 1007
 QY 944 AYPGSGPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVAMMTVEL 1003
 DB 1008 SYNGYPFLFWEQYIGLRHLLIFTSVVLACTFLCAVFLNPWTAGIIVMLALMTVEL 1067
 QY 1004 FCIMGFLGKLSAIPWVILVASVGIGVEFTHVALGFLTTQGSRLNRAHALEHTFAPVT 1063
 DB 1068 FQMMGLIGKLSAVPVWILIASVGIGVEFTHVALAFLTAIGDKRRRAVLAEHMFAPVL 1127
 QY 1064 DCAISTLLGLMLAGSHDFIVRYFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVI-- 1121
 DB 1128 DGAVSTLLGVMLAGSEDFIVRYFAVALITLILGVNLGLVLLPVLLSFFGYPPEVSPA 1187
 QY 1122 ---QMYKESPE-----ILSP-----APQGG 1139
 DB 1188 NGLNELPTSPPEPPSVVRFAMP PGHTHSGSDSDSEYSSQTTVSGLSEELRHVEAQGA 1247
 QY 1140 G-----LRWG-----ASSSLPQSFA 1155
 DB 1248 GGAHQVIVATENPVFAHSTVWHPESRHHPPSNRQOQPHLDGSLPPGROGQQRDRPP 1307
 QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
 DB 1368 ITTVTASAVTVAVHPPVPVPGGRNP 1393

Search completed: November 22, 2004, 07:55:54
 Job time : 89 secs

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